

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 9, 2004, 11:04:11 ; Search time 37.4865 Seconds
(without alignments)
159.920 Million cell updates/sec

Title: US-10-030-485A-6
Sequence: 1 ADSNKTIDEANQRATKML 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | ID | Description |
|------------|-------|---------|-------|--------|--------|--------------------|
| 1 | 93 | 100.0 | 124 | 13 | Q93578 | Q93578 brachydanio |
| 2 | 93 | 100.0 | 143 | 6 | Q9GM34 | Q9GM34 macaca fasc |
| 3 | 93 | 100.0 | 203 | 13 | Q93579 | Q93579 brachydanio |
| 4 | 79 | 84.9 | 206 | 13 | Q8AXM2 | Q8AXM2 xenopus lae |
| 5 | 79 | 84.9 | 206 | 13 | Q8AXM1 | Q8AXM1 xenopus lae |
| 6 | 75 | 80.6 | 214 | 13 | Q7ZVE4 | Q7ZVE4 brachydanio |
| 7 | 71 | 76.3 | 212 | 5 | Q8T3S4 | Q8T3S4 loligo peal |
| 8 | 66 | 71.0 | 204 | 13 | Q8JIS7 | Q8JIS7 xenopus lae |
| 9 | 60 | 64.5 | 210 | 11 | Q70377 | Q70377 rattus norv |
| 10 | 60 | 64.5 | 210 | 11 | Q09044 | Q09044 mus musculu |
| 11 | 60 | 64.5 | 221 | 11 | Q9D3L3 | Q9D3L3 mus musculu |
| 12 | 55 | 59.1 | 210 | 11 | Q35620 | Q35620 mus musculu |
| 13 | 53 | 57.0 | 212 | 5 | Q01389 | Q01389 hirudo medi |
| 14 | 51 | 54.8 | 125 | 5 | Q96576 | Q96576 leucophaea |
| 15 | 50 | 53.8 | 90 | 5 | Q96578 | Q96578 leucophaea |
| 16 | 50 | 53.8 | 191 | 17 | Q8ZY72 | Q8ZY72 Pyrobaculum |

062414 caenorhabdi
Q81kf6 bacillus an
Q812m9 bacillus ce
Q869g6 lymaea sta
Q95zk3 caenorhabdi
Q23081 caenorhabdi
Q85440 pseudomonas
Q85439 pseudomonas
Q85431 pseudomonas
Q85438 pseudomonas
Q81ae0 procamburus
Q81ae0 procamburus
Q3vh76 drosophila
Q44419 strongyloce
Q76338 strongyloce
Q984j1 rhizobium 1
Q9piu7 campylobact
Q9bws6 homo sapien
Q9bys5 homo sapien
Q89q18 bradyrhizob
Q8ck7 homo sapien
Q8y4z2 listeria mo
Q9c014 homo sapien
Q9c013 homo sapien
Q9c012 homo sapien
Q9hat7 homo sapien
Q9ub61 homo sapien
Q8ncr8 homo sapien
Q8fnr8 corynebacte

ALIGNMENTS

RESULT 1
ID Q93578 PRELIMINARY; PRT; 124 AA.

AC Q93578; TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 25, Last annotation update)
DE Synaposome-associated protein 25.1 (Fragment).
GN SNAP25A OR SNAP.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RX MEDLINE=99057281; PubMed=9843147;
RA Risinger C., Salanek B., Soderberg C., Gates M., Postlethwait J.H.,
RA Lathamar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573 (1998).
DR EMBL; AF091593; AAC64289.1;
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR InterPro; IPR000928; SNAP-25.
DR Pfam; PF00835; SNARE-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; t_SNARE; 1.
DR NON_TER 1
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 93; DB 13; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRATKML 19

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Db 103 ADSNKTIDEANORATKML 121
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RESULT 2
Q9GM34 PRELIMINARY; PRT; 143 AA.
AC Q9GM34;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB049852; BAB16738.1; -.
DR InterPro: IPR000928; SNAP-25.
DR InterPro: IPR000727; T_SNARE.
DR Pfam: PF00835; SNAP-25; 1.
DR Pfam: PF05739; SNARE; 1.
DR SMART: SM00397; t_SNARE; 1.
DR PROSITE: PS0192; T_SNARE; 1.
KW Hypothetical protein
SQ SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FE0 CRC64;

Query Match 100.0%; Score 93; DB 6; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANORATKML 19
|||||
Db 122 ADSNKTIDEANORATKML 140
|||||
RESULT 3
Q93579 PRELIMINARY; PRT; 203 AA.
AC Q93579;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
DE 25.2).
GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage."
RL J. Neurosci. Res. 0:0-0(1998).
DR EMBL: AF091594; AAC64290.1; -.
DR EMBL: AF091596; AAC73007.1; -.
DR ZFIN: ZDB-GENE-980526-392; snap25b.
DR InterPro: IPR000928; SNAP-25.
DR InterPro: IPR000727; T_SNARE.
DR Pfam: PF00835; SNAP-25; 1.

Query Match 84.9%; Score 79; DB 13; Length 206;
Best Local Similarity 84.2%; Pred. No. 6.9e-05;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANORATKML 19
|||||
Db 185 ADSNKTIDEANORATKML 203
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RESULT 5
Q8AXM1 PRELIMINARY; PRT; 206 AA.
AC Q8AXM1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNAP25b (Hypothetical protein).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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DR InterPro: IPR000928; SNAP-35.
DR InterPro: IPR000727; T-SNARE.
DR Pfam: PF00835; SNAP-25_1.
DR

| | |
|-----------------------|---|
| RC | TISSUE=Fat; |
| RX | MEDLINE=97312558; PubMed=9168999; |
| RA | Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H., |
| RA | Niki T., Okazawa H., Kubota T., Kasuga M.; |
| RT | "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c."; |
| RL | Biochem. Biophys. Res. Commun. 234:257-262(1997). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=97220227; PubMed=9067602; |
| RA | Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E., |
| RA | Baldini G.; |
| RT | "Synaptobrevin is a novel SNAP-25 related protein expressed in many |
| RL | tissues."; |
| RL | J. Cell Sci. 110:505-513(1997). |
| RN | [3] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=C57BL/6J; TISSUE=Embryo; |
| RX | MEDLINE=21085660; PubMed=11217851; |
| RA | Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., |
| RA | Akaiwa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S., |
| RA | Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., |
| RA | Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R., |
| RA | Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., |
| RA | Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., |
| RA | Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., |
| RA | Schiraldi L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T., |
| RA | Sakai K., Okado T., Furuno M., Aono H., Baldarelli R., Barsh G., |
| RA | Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., |
| RA | Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., |
| RA | Gustincich S., Hill D., Hofmann M., Humé D.A., Mazzarelli J., Mombaerts P., |
| RA | Lyons P., Marchionni L., Mashima J., Muzzarelli J., Sakamoto N., |
| RA | Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., |
| RA | Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., |
| RA | Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., |
| RA | Yanashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., |
| RA | Hayashizaki Y.; |
| RA | "Functional annotation of a full-length mouse cDNA collection."; |
| RL | Nature 409:685-690(2001). |
| DR | EMBL; AB000822; BAA20345.1; - |
| DR | EMBL; U73143; AAB53597.1; - |
| DR | EMBL; AF213257; AAF23503.1; JOINED. |
| DR | EMBL; AF213251; AAF23503.1; JOINED. |
| DR | EMBL; AF213252; AAF23503.1; JOINED. |
| DR | EMBL; AF213253; AAF23503.1; JOINED. |
| DR | EMBL; AF213254; AAF23503.1; JOINED. |
| DR | EMBL; AF213255; AAF23503.1; JOINED. |
| DR | EMBL; AF213256; AAF23503.1; JOINED. |
| DR | EMBL; AK019164; BAB31577.1; - |
| DR | PIR; JC5512; JC5512. |
| DR | MGD; MG1:109356; Snap23. |
| DR | InterPro; IPRO00928; SNAP-25. |
| DR | InterPro; IPRO00727; T SNARE. |
| DR | Pfam; PF00835; SNAP-25; 1. |
| DR | Pfam; PF05739; SNARE; 1. |
| DR | SMART; SM00397; t SNARE; 2. |
| DR | PROSITE; PS50192; T SNARE; 2. |
| SQ | SEQUENCE 210 AA; 23261 MW; 6919E127E16BA2C9 CRC64; |
| Query Match | 64.5%; Score 60; DB 11; Length 210; |
| Best Local Similarity | 63.2%; Pred. No. 0.091; |
| Matches | 12; Conservative |
| Qy | 1 ADSNKTRIDEANORATKML 19 |
| Dd | 190 ADTNKNRIDIANTRAKKLI 208 |
| RESULT 10 | |
| ID | O09044 PRELIMINARY; PRT; 210 AA. |
| AC | O09044 |
| DT | 01-JUL-1997 (TrEMBLrel. 04, Created) |
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) |
| DE | SYNDET (SNAP-23) (Synaptoosomal-associated protein, 23KD). |
| GN | SNAP23 OR SNDT. |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. |
| OX | NCBI_TaxID=10090; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=C57BL/6J; TISSUE=Embryo; |
| RX | MEDLINE=97312558; PubMed=9168999; |
| RA | Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H., |
| RA | Niki T., Okazawa H., Kubota T., Kasuga M.; |
| RT | "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c."; |
| RL | Biochem. Biophys. Res. Commun. 234:257-262(1997). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=97220227; PubMed=9067602; |
| RA | Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E., |
| RA | Baldini G.; |
| RT | "Synaptobrevin is a novel SNAP-25 related protein expressed in many |
| RL | tissues."; |
| RL | J. Cell Sci. 110:505-513(1997). |
| RN | [3] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=C57BL/6J; TISSUE=Embryo; |
| RX | MEDLINE=21085660; PubMed=11217851; |
| RA | Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., |
| RA | Akaiwa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S., |
| RA | Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., |
| RA | Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R., |
| RA | Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., |
| RA | Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., |
| RA | Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., |
| RA | Schiraldi L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T., |
| RA | Sakai K., Okado T., Furuno M., Aono H., Baldarelli R., Barsh G., |
| RA | Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., |
| RA | Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., |
| RA | Gustincich S., Hill D., Hofmann M., Humé D.A., Mazzarelli J., Mombaerts P., |
| RA | Lyons P., Marchionni L., Mashima J., Muzzarelli J., Sakamoto N., |
| RA | Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., |
| RA | Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., |
| RA | Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., |
| RA | Yanashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., |
| RA | Hayashizaki Y.; |
| RA | "Functional annotation of a full-length mouse cDNA collection."; |
| RL | Nature 409:685-690(2001). |
| DR | EMBL; AB000822; BAA20345.1; - |
| DR | EMBL; U73143; AAB53597.1; - |
| DR | EMBL; AF213257; AAF23503.1; JOINED. |
| DR | EMBL; AF213251; AAF23503.1; JOINED. |
| DR | EMBL; AF213252; AAF23503.1; JOINED. |
| DR | EMBL; AF213253; AAF23503.1; JOINED. |
| DR | EMBL; AF213254; AAF23503.1; JOINED. |
| DR | EMBL; AF213255; AAF23503.1; JOINED. |
| DR | EMBL; AF213256; AAF23503.1; JOINED. |
| DR | EMBL; AK019164; BAB3157 |

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RESULT 11
Q9D3L3
ID Q9D3L3 PRELIMINARY; PRT; 221 AA.
AC Q9D3L3
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptoosomal-associated protein, 23kD.
GN SNAP23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017311; BAB30686.1; -.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 221 AA; 24550 MW; 368862BE7232DEFB CRC64;

Query Match 64.5%; Score 60; DB 11; Length 221;
Best Local Similarity 63.2%; Pred. No. 0.096; Mismatches 4; Indels 0; Gaps 0;
Matches 12; Conservative 3;

QY 1 ADSNKTIDEANQRATKML 19
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Db 201 ADTNKNEIDIANTRAKLI 219
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RESULT 12
O35620
ID O35620 PRELIMINARY; PRT; 210 AA.
AC O35620;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 23kDa synaptoosomal associated protein.
GN SNAP23 OR MSNAP-23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Olken S.K., Doerre S., Corley R.B.;
RA Olken S.K., Doerre S., Corley R.B.;
RT "SNARE expression in mouse plasma cells.";

Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF007169; AAB62932.1; -.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 210 AA; 23277 MW; FB752FB58D5AE6D9 CRC64;

Query Match 59.1%; Score 55; DB 11; Length 210;
Best Local Similarity 57.9%; Pred. No. 0.6; Mismatches 5; Indels 0; Gaps 0;
Matches 11; Conservative 3;

QY 1 ADSNKTIDEANQRATKML 19
||| ||| ||| ||| ||| |||
Db 190 ADTNKNEIDIANTRPKLI 208
||| ||| ||| ||| ||| |||

RESULT 13
O01389
ID O01389 PRELIMINARY; PRT; 212 AA.
AC O01389;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNAP-25 homolog.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Ancyrobrellida; Hirudiniformes; Hirudinidae; Hirudo.
ON NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nerve cord;
RX MEDLINE=97197869; PubMed=9045719;
RA Bruns D., Engers S., Yang C., Ossig R., Jeromin A., Jahn R.;
RT "Inhibition of transmitter release correlates with the proteolytic
RT activity of tetanus toxin and botulinus toxin A in individual cultured
RT synapses of Hirudo medicinalis.";
RL J. Neurosci. 17:1898-1910(1997).
DR EMBL; U85806; AAC47499.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 212 AA; 23802 MW; 8FF591DF32A4FCB6 CRC64;

Query Match 57.0%; Score 53; DB 5; Length 212;
Best Local Similarity 58.8%; Pred. No. 1.3; Mismatches 2; Indels 0; Gaps 0;
Matches 10; Conservative 5;

QY 3 SNKTIDEANQRATKML 19
||| ||| ||| ||| ||| |||
Db 194 SNQIRISDANKRASKIL 210
||| ||| ||| ||| ||| |||

RESULT 14
O96576
ID O96576 PRELIMINARY; PRT; 125 AA.
AC O96576;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptoosome-associated protein SNAP-25-3 (Fragment).
GN SNAP-3.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
ON NCBI_TaxID=6988;

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Tue Mar 9 16:44:00 2004

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=9259578; PubMed=10327594;
RA  Johard H.A., Risinger C., Nasseel D.R., Larhammar D.;
RT  "The highly conserved synapse protein SNAP-25 displays sequence
RL  variability in the cockroach Leucophaea maderae.";
RT  Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
RL  EMBL; AF091600; AAC69876.1; -.
DR  InterPro; IPR000928; SNAP-25.
DR  InterPro; IPR000727; T_SNARE.
DR  Pfam; PF00835; SNAP-25; 1.
DR  Pfam; PF05739; SNARE; 1.
DR  SMART; SM00397; t_SNARE; 1.
DR  PROSITE; PS50192; T_SNARE; 1.
FT  NON_TER 1
SQ  SEQUENCE 125 AA; 13985 MW; 72B032879858C316 CRC64;

Query Match      54.8%; Score 51; DB 5; Length 125;
Best Local Similarity 52.6%; Pred. No. 1.5;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY  1 ADSNKTTRIDEANQATKML 19
DB  105 AESNEERIKVANQASNIM 123
      :||: || |||||: :
      :||: || |||||: :

RESULT 15
O96578
ID  O96578      PRELIMINARY;      PRT;      90 AA.
AC  O96578;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DT  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  Synapsome-associated protein SNAP-25-5 (Fragment).
GN  SNAP-5.
OS  Leucophaea maderae (Madeira cockroach).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC  Blaberidae; Leucophaea.
OX  NCBI TaxID=6988;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9259578; PubMed=10327594;
RA  Johard H.A., Risinger C., Nasseel D.R., Larhammar D.;
RT  "The highly conserved synapse protein SNAP-25 displays sequence
RL  variability in the cockroach Leucophaea maderae.";
RT  Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
RL  EMBL; AF091602; AAC69878.1; -.
DR  InterPro; IPR000928; SNAP-25.
DR  InterPro; IPR000727; T_SNARE.
DR  Pfam; PF00835; SNAP-25; 1.
DR  Pfam; PF05739; SNARE; 1.
DR  SMART; SM00397; t_SNARE; 1.
DR  PROSITE; PS50192; T_SNARE; 1.
FT  NON_TER 1
SQ  SEQUENCE 90 AA; 10136 MW; E502D8954676E9F7 CRC64;

Query Match      53.8%; Score 50; DB 5; Length 90;
Best Local Similarity 57.9%; Pred. No. 1.6;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY  1 ADSNKTTRIDEANQATKML 19
DB  71 AESNEERIKVANQAHNLL 89
      :||: || |||||: :
      :||: || |||||: :

Search completed: March 9, 2004, 11:09:36
Job time : 38.4865 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 10:58:06 ; Search time 10.7838 Seconds
(without alignments)
91.743 Million cell updates/sec

Title: US-10-030-485A-6

Perfect score: 93
Sequence: 1 ADSNKTRIDEANORATKML 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 93 | 100.0 | 203 | 1 SN2B CARAU | P36978 carassius a |
| 2 | 93 | 100.0 | 204 | 1 SN2A CARAU | P36977 carassius a |
| 3 | 93 | 100.0 | 206 | 1 SN25 HUMAN | P13795 homo sapien |
| 4 | 70 | 75.3 | 210 | 1 SN25 TORMA | P36976 torpedo nar |
| 5 | 56 | 60.2 | 211 | 1 SN25 HUMAN | O00161 homo sapien |
| 6 | 47 | 50.5 | 212 | 1 SN25 DROME | P36975 drosophila |
| 7 | 42 | 45.2 | 83 | 1 MULI PSEAE | P11221 pseudomonas |
| 8 | 42 | 45.2 | 420 | 1 YEO9 YEAST | P40038 saccharomyc |
| 9 | 41.5 | 44.6 | 181 | 1 ARF2 MOUSE | P16500 mus musculu |
| 10 | 41 | 44.1 | 494 | 1 PR31 YEAST | P49704 saccharomyc |
| 11 | 40 | 43.0 | 252 | 1 YC87 STAEF | O8csb6 acaphylococ |
| 12 | 40 | 43.0 | 975 | 1 KINH DROME | P17210 drosophila |
| 13 | 39.5 | 42.5 | 181 | 1 ARF1 DICDI | O00909 dictyosteli |
| 14 | 39 | 41.9 | 294 | 1 CAL2 PARTE | Q94715 paramecium |
| 15 | 39 | 41.9 | 313 | 1 MRAW SHEVI | Q9f1n8 shewanella |
| 16 | 39 | 41.9 | 438 | 1 TAP1 DROME | Q24306 drosophila |
| 17 | 39 | 41.9 | 480 | 1 ORP2 HUMAN | Q9h1p3 homo sapien |
| 18 | 39 | 41.9 | 970 | 1 K852 HUMAN | Q9yex9 homo sapien |
| 19 | 38.5 | 41.4 | 200 | 1 SWRI SERLI | P52989 serratia li |
| 20 | 38.5 | 41.4 | 918 | 1 YNJB CABEL | P34487 caenorhabdi |
| 21 | 38.5 | 41.4 | 1337 | 1 DEXT STRDO | P39653 streptococc |
| 22 | 38 | 40.9 | 151 | 1 SVB2 RHIME | Q923q1 rhizobium m |
| 23 | 38 | 40.9 | 204 | 1 TIPP2 RAT | P50411 rattus norv |
| 24 | 38 | 40.9 | 244 | 1 I431 ECHGR | Q90408 echinococcu |
| 25 | 38 | 40.9 | 244 | 1 I431 ECHMU | Q24902 echinococcu |
| 26 | 38 | 40.9 | 251 | 1 SN29 ARATH | Q9sd96 arabidopsis |
| 27 | 38 | 40.9 | 263 | 1 SN30 ARATH | Q9lmg8 arabidopsis |
| 28 | 38 | 40.9 | 385 | 1 MTLD LACPL | O8azsl lactobacill |
| 29 | 38 | 40.9 | 473 | 1 GATE MYCFU | Q98r09 mycoplasma |
| 30 | 38 | 40.9 | 476 | 1 ANG1 SHEEP | P20757 ovine aries |
| 31 | 38 | 40.9 | 558 | 1 YBAL ECOLI | P39830 escherichia |
| 32 | 38 | 40.9 | 586 | 1 YEJM ECOLI | P33922 escherichia |
| 33 | 38 | 40.9 | 675 | 1 H57M_PEA | P37900 pisum sativ |

RESULT 1
SN2B CARAU ID SN2B CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptoosomal-associated protein 25B (SNAP-25B).
GN SNAP-B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammer D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602 (1993).
CC -|- FUNCTION: May play an important role in the synaptic function of vesicle docking and membrane fusion.
CC -|- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -|- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -|- SIMILARITY: Belongs to the SNAP-25 family.
CC -|- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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CC -----
CC EMBL: L22976; AAA1538.1; --
CC PIR: I50481; I50481.
CC InterPro: IPR000928; SNAP-25.
CC InterPro: IPR000727; T-SNARE.
CC Pfam: PF00835; SNAP-25; 1.
CC Pfam: PF05739; SNARE; 1.
CC SMART: SM00397; t-SNARE; 2.
CC PROSITE: PS50192; T-SNARE; 2.
CC Synaptoosome; Neurone; Repeat; Coiled coil; Multigene family.
KW Synaptoosome; Neurone; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CYS-RICH.
FT CARBOHYD 77 77 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 203 AA; 22664 MW; 8DFBEBED37B6D7 CRC64;

34 38 40.9 675 1 UVRB NEIMA P56996 neisseria m
35 38 40.9 675 1 UVRB NEIME O33395 neisseria m
36 38 40.9 693 1 SYGB BACHD Q9kd48 bacillus ba
37 38 40.9 1966 1 MYSB CABEL P02586 caenorhabdi
38 37.5 40.3 403 1 CID DROYA O77027 drosophila
39 37.5 40.3 1397 1 CID DROME P19538 drosophila
40 37 39.8 241 1 RRPB HRSV P14156 human respi
41 37 39.8 241 1 RRPB HRSVA P03421 human respi
42 37 39.8 241 1 RRPB HRSVL P12579 human respi
43 37 39.8 266 1 PR11 MYCPN Q07350 saccharomyc
44 37 39.8 329 1 YE57 MYCPN P75326 mycoplasma
45 37 39.8 372 1 YQIG BACSU P54524 bacillus su

ALIGNMENTS

Query Match 100.0%; Score 93; DB 1; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSNKTTRIDEANQATKML 19
 DB 182 ADSNKTTRIDEANQATKML 200

RESULT 2

SN2A_CARAU STANDARD; PRT; 204 AA.
 AC P36977;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Synaptosomal-associated protein 25A (SNAP-25A).
 GN SNAP-A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]_TaxID=7957;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94068448; PubMed=8248151;
 RA Risinger C., Larhammar D.;
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
 RT goldfish";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602 (1993).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 CC specific neuronal systems. Associates with proteins involved in
 CC vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 CC the nerve terminal.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC
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 CC
 CC EMBL; L22973; AAA16537.1; -;
 DR PIR; I50480.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; t-SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS50192; t-SNARE; 2.
 KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.
 FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOLGY 1.
 FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOLGY 2.
 FT DOMAIN 85 92 CYS-RICH.
 SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;

Query Match 100.0%; Score 93; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSNKTTRIDEANQATKML 19
 DB 183 ADSNKTTRIDEANQATKML 201

RESULT 3

SN25_HUMAN

SN25_HUMAN STANDARD; PRT; 206 AA.
 AC P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
 GN SNAP25 OR SNAP.
 OS Homo sapiens (Human).
 OS Macaca mulatta (Rhesus macaque).
 OS Mus musculus (Mouse).
 OS Rattus norvegicus (Rat), and
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606; 9544; 10090; 10116; 9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94156217; PubMed=8112622;
 RA Bark I.C., Wilson M.C.;
 RT "Human cDNA clones encoding two different isoforms of the nerve
 RT terminal protein SNAP-25";
 RL Gene 139:291-292 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94333829; PubMed=8056350;
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
 RT "Cloning and sequence analysis of the human SNAP25 cDNA";
 RL Gene 145:313-314 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC SPECIES=Human; TISSUE=Skeletal muscle;
 RX MEDLINE=96322494; PubMed=8760387;
 RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,
 RA Frenkel M.J., Ward C.W.;
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25
 RT (synaptosomal-associated protein 25) A and B isoforms in addition to
 RT syntaxin 4 and synaptobrevins 1 and 2";
 RL Biochem. J. 317:945-954 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.W., Beare D.M., Brown A.J.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvaish M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McJay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Beck S.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871 (2001).
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Human; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleto M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=M.mullatta; TISSUE=Hippocampus;
 RX Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=BA1B/C;
 RX MEDLINE=90078337; PubMed=2592413;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein,
 RT SNAP-25, differentially expressed by neuronal subpopulations.";
 RL J. Cell Biol. 109:3039-3052(1989).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=ILIS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Siketa J.M.;
 RT "High-throughput sequence identification of gene coding variants
 RT within alcohol-related QTLs.";
 RL Mamm. Genome 12:657-663(2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynchaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
 RA Strausberg R.L.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Cat;
 RA Kataoka M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Brain;
 RA Cho A.R., You K.H.;
 RT "Cloning of the SNAP-25 gene from a rat brain cDNA library.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Brain;
 RX MEDLINE=99155074; PubMed=10037470;
 RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
 RT "SNARE complex proteins, including the cognate pair VAMP-2 and
 RT syntaxin-4, are expressed in cultured oligodendrocytes.";
 RL J. Neurochem. 72:988-998(1999).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; TISSUE=Retina;
 RX MEDLINE=91126080; PubMed=1992470;
 RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
 RA Wilson M.C.;
 RT "Expression of a conserved cell-type-specific protein in nerve
 RT terminals coincides with synaptogenesis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
 RN [15]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Chicken;
 RX MEDLINE=93389738; PubMed=8377193;
 RA Bark I.C.;
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
 RT encoding distinct isoforms of the protein.";
 RL J. Mol. Biol. 233:67-76(1993).
 RN [16]
 RP PALMITOYLATION.
 RC SPECIES=Brain;
 RX MEDLINE=91100552; PubMed=1281490;
 RA Hess D.F., Slater T.M., Wilson M.C., Skene J.H.P.;
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
 RT methionine-rich polypeptide in rapid axonal transport and a major

Query Match 100.0%; Score 93; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQRATKML 19
 Db 185 ADSNKTIDEANQRATKML 203

RESULT 4
 ID SN25 TORMA STANDARD; PRT; 210 AA.
 AC P36976;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25).
 OS Torpedo marmorata (Marbled electric ray).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 CC Elasmobranchii; Squalia; Hyposqualia; Priistioraja; Batoida;
 CC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
 CC NCBI_TaxID=7788;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
 RC TISSUE=Electric lobe;
 RA MEDLINE=94043281; PubMed=8226991;
 RX Rinsinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
 (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
 RL J. Biol. Chem. 268:24408-24414 (1993).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 CC specific neuronal systems. Associates with proteins involved in
 CC vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 CC the nerve terminal.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC -----
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 CC -----
 CC EMBL; L22020; AAA49284.1; -;
 DR PIR; I50552; I50552.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; t-SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS50192; t-SNARE; 2.
 KW Synaptosome; Neurone; Repeat; Coiled coil.
 FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOLOGY 1.
 FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOLOGY 2.
 FT DOMAIN 88 96 CYS-RICH.
 SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;
 Query Match 75.3%; Score 70; DB 1; Length 210;
 Best Local Similarity 77.8%; Pred. No. 0.00019;
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 DSNKTRIDEANQRATKML 19
 Db 193 DMNKARIDEANKHATKML 210
 ||| ||||| |||||
 ||| ||||| |||||
 RESULT 5
 SN23 HUMAN STANDARD; PRT; 211 AA.
 ID SN23 HUMAN STANDARD; PRT; 211 AA.
 AC O00161; O00162; O13602;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane fusion
 DE protein SNAP-23).
 GN SNAP23.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
 RC TISSUE=B-cell;
 RX MEDLINE=96278745; PubMed=8663154;
 RA Ravichandran V., Chawla A., Roche P.A.;
 RT "Identification of a novel syntaxin- and synaptobrevin/VAMP-binding
 RT protein, SNAP-23, expressed in non-neuronal tissues.";

J. Biol. Chem. 271:13300-13303 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-23A AND SNAP-23B).
 RC TISSUE=Neutrophils;
 RX MEDLINE=97224437; PubMed=9070898;
 RA Mollinedo F., Lazo P.A.;
 RT "Identification of two isoforms of the vesicle-membrane fusion protein
 RT SNAP-23 in human neutrophils and HL-60 cells.";
 RL Biochem. Biophys. Res. Commun. 231:808-812 (1997).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RA Nadel M., Area E., Mollinedo F., Estivill X., Lazo P.A.;
 RT "Xon organization and chromosomal localization of human synaptosomal
 RT associated protein-23 (SNAP-23) gene and generation of isoforms by
 RT alternative splicing";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
 RC TISSUE=Cervix, Placenta, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF THE HIGH AFFINITY RECEPTOR FOR
 CC OF TRANSPORT VESICLE DOCKING AND FUSION.
 CC -!- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND
 CC SYNAPTOBREVIN/VAMPs.
 CC -!- SUBCELLULAR LOCATION: MAINLY LOCALIZED TO THE PLASMA MEMBRANE.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=SNAP-23a;
 CC IsoId=O00161-1; Sequence=Displayed;
 CC Name=SNAP-23b;
 CC IsoId=O00161-2; Sequence=VSP_006187, VSP_006188;
 CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS WHERE FOUND IN
 CC PLACENTA.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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 CC -----
 CC EMBL; U55936; AAC50537.1; -;
 DR EMBL; Y09567; CAA70760.1; -;
 DR EMBL; Y09568; CAA70761.1; -;
 DR EMBL; AJ011915; CAA09864.1; -;
 DR EMBL; BC000148; AAH00148.1; -;
 DR EMBL; BC003686; AAH03686.1; -;
 DR EMBL; BC022890; AAH22890.1; -;
 DR FIR; JC5296; JC5296.

assembly. ";

RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).

CC -!- FUNCTION: May play an important role in the synaptic function of

CC specific neuronal systems. Associates with proteins involved in

CC vesicle docking and membrane fusion.

CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of

CC the nerve terminal.

CC -!- TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA.

CC -!- SIMILARITY: Belongs to the SNAP-25 family.

CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC

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CC

DR EMBL; L22021; AAA16059.1; -

DR EMBL; U81153; AAB39757.1; -

DR EMBL; U81147; AAB39757.1; JOINED.

DR EMBL; U81148; AAB39757.1; JOINED.

DR EMBL; U81149; AAB39757.1; JOINED.

DR EMBL; U81150; AAB39757.1; JOINED.

DR EMBL; U81151; AAB39757.1; JOINED.

DR EMBL; U81152; AAB39757.1; JOINED.

DR EMBL; U81152; AAB39757.1; JOINED.

DR FlyBase; FBgn0011288; Snap25.

DR GO; GO:0005886; C:plasma membrane; NAS.

DR GO; GO:0005486; F:t-SNARE activity; NAS.

DR GO; GO:0007269; P:neurotransmitter secretion; NAS.

DR GO; GO:0016081; P:synaptic vesicle docking; NAS.

DR GO; GO:0016083; P:synaptic vesicle fusion; NAS.

DR InterPro; IPR000928; SNAP-25.

DR InterPro; IPR000727; T-SNARE.

DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.

DR SMART; SM00397; t-SNARE; 2.

DR PROSITE; PS00192; T-SNARE; 2.

DR KW Synaptosome; Neurope; Repeat; Coiled coil.

FT DOMAIN 26 88 T-SNARE COILED-COIL HOMOMOLOGY 1.

FT DOMAIN 148 210 T-SNARE COILED-COIL HOMOMOLOGY 2.

FT DOMAIN 91 99 CVS-RICH.

FT SEQUENCE 212 AA; 23685 MW; BDC90649A1AF3AC8 CRC64;

Query Match 50.5%; Score 47; DB 1; Length 212;

Best Local Similarity 55.6%; Pred. No. 1.3;

Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 DSNKTRIDEANORATKML 19

DB 194 ESNEARIANORAHQLL 211

RESULT 7

MULTI PSEAE

ID MULTI PSEAE STANDARD; PRT; 83 AA.

AC P11221;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Major outer membrane lipoprotein precursor (Murein-lipoprotein)

DE (Lipoprotein I).

GN OPR1 OR PA2853.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Isolate PA2;

RX MEDLINE=89315294; PubMed=2473376; Guyonvarch A., Kammerer B.,

RA Cornelis P., Boula A., Belarbi A., Guyonvarch A., Kammerer B.,

RT

PIR; JC5297; JC5297.

Genew; HGNC:11131; SNAP23.

MIM; 602534; -

GO; GO:0005886; C:plasma membrane; TAS.

GO; GO:0005803; C:secretory vesicle; TAS.

GO; GO:0006944; P:membrane fusion; TAS.

GO; GO:0006903; P:nonselective vesicle targeting; TAS.

GO; GO:0006892; P:post-Golgi transport; TAS.

InterPro; IPR000928; SNAP-25.

InterPro; IPR000727; T-SNARE.

Pfam; PF00835; SNAP-25; 1.

Pfam; PF05739; SNARE; 1.

SMART; SM00397; t-SNARE; 2.

PROSITE; PS00192; T-SNARE; 2.

Protein transport; Synaptosome; Coiled coil; Alternative splicing;

Membrane; Repeat.

DOMAIN 14 76 T-SNARE COILED-COIL HOMOMOLOGY 1.

DOMAIN 146 208 T-SNARE COILED-COIL HOMOMOLOGY 2.

DOMAIN 89 89 R -> S (in isoform SNAP-23b).

VARSPLIC 89 89 /FTid-VSP 006187.

VARSPLIC 90 142 Missing (in isoform SNAP-23b).

DOMAIN 14 76 T-SNARE COILED-COIL HOMOMOLOGY 1.

DOMAIN 146 208 T-SNARE COILED-COIL HOMOMOLOGY 2.

DOMAIN 89 89 R -> S (in isoform SNAP-23b).

VARSPLIC 89 89 /FTid-VSP 006187.

VARSPLIC 90 142 Missing (in isoform SNAP-23b).

Query Match 60.2%; Score 56; DB 1; Length 211;

Best Local Similarity 57.9%; Pred. No. 0.041;

Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ADSNKTRIDEANORATKML 19

DB 191 ADTNDRIDIANARAKKLI 209

RESULT 6

SN25_DROME

ID SN25_DROME STANDARD; PRT; 212 AA.

AC P36975;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Synaptosomal-associated protein 25 (SNAP-25).

DE SNAP25.

GN Drosophila melanogaster (Fruit fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

[1]

SEQUENCE FROM N.A.

TISSUE=Head;

RC MEDLINE=94043281; PubMed=8226991;

Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,

Nassel D., Pierboni V.A., Brodin L., Larhammar D.;

"Evolutionary conservation of synaptosome-associated protein 25 kDa

(SNAP-25) shown by Drosophila and Torpedo cDNA clones.;"

J. Biol. Chem. 268:24408-24414 (1993).

[2]

SEQUENCE FROM N.A.

MDLINE=97417485; PubMed=9272858;

Risinger C., Deitcher D.L., Lundell I., Schwarz T.L., Larhammar D.;

"Complex gene organization of synaptic protein SNAP-25 in Drosophila

melanogaster.;"

Gene 194:169-177 (1997).

[3]

SEQUENCE FROM N.A.

STRAIN=Berkely;

MDLINE=22426071; PubMed=12537574;

Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,

Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,

Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,

Karpen G.H.;

"Heterochromatic sequences in a Drosophila whole-genome shotgun

RT

RA Hannaert V., Hubert J.-C.;
RT "Cloning and analysis of the gene for the major outer membrane
RL lipoprotein from *Pseudomonas aeruginosa*.";
RN Mol. Microbiol. 3:421-428 (1989).
RP SEQUENCE FROM N.A.
RX MEDLINE=89327122; PubMed=2502533;
RA Duchene M., Barron C., Schweizer A., von Sprecht B.-U., Dondey H.;
RT "Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular
RL cloning, sequence, and expression in *Escherichia coli*.";
RN J. Bacteriol. 171:4130-4137 (1989).
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RA Saint-Onge A., Roney F., Lebel P., Masson L., Brousseau R.;
RT "Specificity of the *Pseudomonas aeruginosa* PA01 lipoprotein I gene as
RL a DNA probe and PCR target region within the *Pseudomonadaceae*.";
RN J. Gen. Microbiol. 138:733-741 (1992).
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.W.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
RL opportunistic pathogen";
RN Nature 406:959-964 (2000).
CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
anchor.
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DR EMBL; X13748; CAA32013.1; -;
DR EMBL; M25761; AAA25880.1; -;
DR EMBL; X58714; CAA41550.1; -;
DR EMBL; A07695; CAA00707.1; -;
DR EMBL; AE004712; AAG06241.1; -;
DR PIR; A33854; A33854.
DR InterPro; IPR000437; Prok lipoprot S.
DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
FT SIGNAL 1 19
FT CHAIN 20 83 MAJOR OUTER MEMBRANE LIPOPROTEIN.
FT LIPID 20 20 N-palmitoyl cysteine.
FT LIPID 20 20 S-diacylglycerol cysteine.
SQ SEQUENCE 83 AA; 8635 MW; E87F52B8E804DBA4 CRC64;
Query Match 45.2%; Score 42; DB 1; Length 83;
Best Local Similarity 72.7%; Pred. No. 3.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 9 DEANORATKML 19
DB 67 DEANERALRML 77
RESULT 8
YEO9 YEAST
AC P40036;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 47.0 kDa protein in PET117-CWI intergenic region.
GN YER059W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RC MEDLINE=97313264; PubMed=9169868;
RA Darioch R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Atriou F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome V";
RN Nature 387:78-81 (1997).
CC -!- SIMILARITY: TO YEAST YIL050W.
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DR EMBL; U18813; AAB64595.1; -;
DR PIR; S50562; S50562.
DR GenOnline; I39139; -;
DR SGD; S0000861; PCL6.
DR GO; GO:0005979; P:regulation of glycogen biosynthesis; IGI.
DR GO; GO:0005981; P:regulation of glycogen catabolism; IGI.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 47007 MW; BD8A0C7A501C94E5 CRC64;
Query Match 45.2%; Score 42; DB 1; Length 420;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 3 SNKTRIDEANQRATKM 18
DB 283 SNESLQKNGRQDKM 298
RESULT 9
ARF2 MOUSE
ID ARF2 MOUSE STANDARD; PRT; 181 AA.
AC P16500; P10947;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE ADP-ribosylation factor 2.
OS ARF2.
OS Mus musculus (Mouse).
OS Rattus norvegicus (Rat), and
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090, 10116, 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RX MEDLINE=88289746; PubMed=3135549;
RA Price S.R., Nightingale M., Teal S.-C., Williamson K.C., Adamik R.,
RA Chen H.-C., Moss J., Vaughan M.;
RT "Guanine nucleotide-binding proteins that enhance cholera toxin ADP-
RT ribosyltransferase activity: nucleotide and deduced amino acid
RT sequence of an ADP-ribosylation factor cDNA";
RN Proc. Natl. Acad. Sci. U.S.A. 85:5488-5491 (1988).

```

[2]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Bovine; TISSUE=Retina;
RX  MEDLINE=93186792; PubMed=8444865;
RA  Serventi I.M., Cavanaugh E., Moss J., Vaughan M.;
RT  "Characterization of the gene for ADP-ribosylation factor (ARF) 2, a
RT  developmentally regulated, selectively expressed member of the ARF
RT  family of approximately 20-kDa guanine nucleotide-binding proteins.";
RL  J. Biol. Chem. 268:4863-4872(1993).
[3]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Rat; TISSUE=Brain;
RA  Nightingale M.S., Price S.R., Tsuchiya M., Moss J., Vaughan M.;
RL  Submitted (XX-1994) to the EMBL/GenBank/DBJ databases.
[4]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Mouse; STRAIN=ICR; TISSUE=Brain;
RX  MEDLINE=97103475; PubMed=8947846;
RA  Hosaka M., Toda K., Takatsu H., Torii S., Murakami K., Nakayama K.;
RT  "Structure and intracellular localization of mouse ADP-ribosylation
RT  factors type 1 to type 6 (ARF1-ARF6).";
RL  J. Biochem. 120:813-819(1996).
[5]
RN  SEQUENCE FROM N.A.
RC  FUNCTION: GTP-binding protein that functions as an allosteric
RC  activator of the cholera toxin catalytic subunit, an ADP-
RC  ribosyltransferase. Involved in protein trafficking; may modulate
CC  vesicle budding and uncoupling within the Golgi apparatus.
CC  -!- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.
CC
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
DR  EMBL; J03794; AAA30383.1; -
DR  EMBL; M88287; AAA30754.1; -
DR  EMBL; M88292; AAA18982.1; -
DR  EMBL; M88293; AAA18982.1; JOINED.
DR  EMBL; M88290; AAA18982.1; JOINED.
DR  EMBL; M88291; AAA18982.1; JOINED.
DR  EMBL; L12381; AAA40686.1; -
DR  EMBL; D87899; BAA13491.1; -
DR  EMBL; A45422; A45422.
DR  PIR; JC4946; JC4946.
DR  HSSP; P32889; IHUR.
DR  MGD; MG1:99595; Arf2.
DR  InterPro; IPR006688; ARF.
DR  InterPro; IPR006689; ARF/SAR.
DR  InterPro; IPR001806; Ras trnsfrmg.
DR  InterPro; IPR005225; Small_GTP.
DR  Pfam; PF00025; arf; 1.
DR  PRINTS; PR00449; RASTRNSFRMG.
DR  PRINTS; PR00328; SARIGTPBP.
DR  SMART; SM00177; ARF; 1.
DR  TIGRFAMs; TIGR00231; small_GTP; 1.
DR  PROSITE; PS01019; ARF; 1.
KW  GTP-binding; Multigene family; Protein transport; Golgi stack.
FT  NP BIND 24 31 GTP (BY SIMILARITY).
FT  NP BIND 67 71 GTP (BY SIMILARITY).
FT  NP BIND 126 129 GTP (BY SIMILARITY).
SQ  SEQUENCE 181 AA; 20746 MW; 95BE17A962B83016 CRC64;

Query Match 44.6%; Score 41.5; DB 1; Length 181;
Best Local Similarity 47.4%; Pred. No. 8.8;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 2 DSN-KTRIDEANQRATKML 19
Db 93 DSNDRVNEARELTRML 111

[2]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Bovine; TISSUE=Retina;
RX  MEDLINE=93186792; PubMed=8444865;
RA  Serventi I.M., Cavanaugh E., Moss J., Vaughan M.;
RT  "Characterization of the gene for ADP-ribosylation factor (ARF) 2, a
RT  developmentally regulated, selectively expressed member of the ARF
RT  family of approximately 20-kDa guanine nucleotide-binding proteins.";
RL  J. Biol. Chem. 268:4863-4872(1993).
[3]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Rat; TISSUE=Brain;
RA  Nightingale M.S., Price S.R., Tsuchiya M., Moss J., Vaughan M.;
RL  Submitted (XX-1994) to the EMBL/GenBank/DBJ databases.
[4]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Mouse; STRAIN=ICR; TISSUE=Brain;
RX  MEDLINE=97103475; PubMed=8947846;
RA  Hosaka M., Toda K., Takatsu H., Torii S., Murakami K., Nakayama K.;
RT  "Structure and intracellular localization of mouse ADP-ribosylation
RT  factors type 1 to type 6 (ARF1-ARF6).";
RL  J. Biochem. 120:813-819(1996).
[5]
RN  SEQUENCE FROM N.A.
RC  FUNCTION: GTP-binding protein that functions as an allosteric
RC  activator of the cholera toxin catalytic subunit, an ADP-
RC  ribosyltransferase. Involved in protein trafficking; may modulate
CC  vesicle budding and uncoupling within the Golgi apparatus.
CC  -!- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC
DR  EMBL; J03794; AAA30383.1; -
DR  EMBL; M88287; AAA30754.1; -
DR  EMBL; M88292; AAA18982.1; -
DR  EMBL; M88293; AAA18982.1; JOINED.
DR  EMBL; M88290; AAA18982.1; JOINED.
DR  EMBL; M88291; AAA18982.1; JOINED.
DR  EMBL; L12381; AAA40686.1; -
DR  EMBL; D87899; BAA13491.1; -
DR  EMBL; A45422; A45422.
DR  PIR; JC4946; JC4946.
DR  HSSP; P32889; IHUR.
DR  MGD; MG1:99595; Arf2.
DR  InterPro; IPR006688; ARF.
DR  InterPro; IPR006689; ARF/SAR.
DR  InterPro; IPR001806; Ras trnsfrmg.
DR  InterPro; IPR005225; Small_GTP.
DR  Pfam; PF00025; arf; 1.
DR  PRINTS; PR00449; RASTRNSFRMG.
DR  PRINTS; PR00328; SARIGTPBP.
DR  SMART; SM00177; ARF; 1.
DR  TIGRFAMs; TIGR00231; small_GTP; 1.
DR  PROSITE; PS01019; ARF; 1.
KW  GTP-binding; Multigene family; Protein transport; Golgi stack.
FT  NP BIND 24 31 GTP (BY SIMILARITY).
FT  NP BIND 67 71 GTP (BY SIMILARITY).
FT  NP BIND 126 129 GTP (BY SIMILARITY).
SQ  SEQUENCE 181 AA; 20746 MW; 95BE17A962B83016 CRC64;

Query Match 44.6%; Score 41.5; DB 1; Length 181;
Best Local Similarity 47.4%; Pred. No. 8.8;
Matches 9; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 2 DSN-KTRIDEANQRATKML 19
Db 93 DSNDRVNEARELTRML 111
```

```

RESULT 10
PR31_YEAST STANDARD; PRT; 494 AA.
AC P49704;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pre-mRNA splicing factor PRP31.
GN PRP31 OR YGR091W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184869; PubMed=8604353;
RA Weidenhammer E.M., Singh M., Ruiz-Noriega M., Woolford J.L. Jr.;
RT "The PRP31 gene encodes a novel protein required for pre-mRNA
RT splicing in Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 24:1164-1170(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Wedler H., Scharfe M., Wedler E., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for pre-mRNA splicing.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC
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CC  or send an email to license@isb-sib.ch).
CC
DR  EMBL; U31970; AAA74984.1; -
DR  EMBL; Z72876; CAA97094.1; -
DR  PIR; S64386; S64386.
DR  GerMOnline; 141403; -.
DR  SGD; S0003323; PRP31.
DR  GO; GO:0030532; C:small nuclear ribonucleoprotein complex; IDA.
DR  GO; GO:0008248; F:pre-mRNA splicing factor activity; IPI.
DR  GO; GO:0006371; P:mRNA splicing; IPI.
DR  InterPro; IPR002687; Nop.
DR  Pfam; PF01798; Nop; 1.
DR  ProDom; PD004104; Nop; 1.
KW mRNA processing; mRNA splicing; Nuclear protein.
FT CONFLICT 361 394 TNPKEIGENLGSTREKNSDYRMSDNVYKIGWLA ->
FT DQPKKXRGKRGKRYKFKFSLSHVQLQNRMEFG (IN
FT REF. 2).
SQ SEQUENCE 494 AA; 55967 MW; 1C320B8630EEF5C8 CRC64;

Query Match 44.1%; Score 41; DB 1; Length 494;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 KTRIDEANQRATKML 19
Db 442 KHRISEANQQADEF 456

RESULT 11
YC87_STAEP STANDARD; PRT; 252 AA.
AC Q8CS56;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0271 protein SEI287.
GN SEI287.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qian Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
CC -1- SIMILARITY: Belongs to the UPF0271 (lamB) family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE016748; AA004886.1; -
CC HAMAP; MF 00691; -; 1.
CC InterPro; IPR005501; Lamb_YcsF.
CC Pfam; PF03746; Lamb_YcsF.1
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 252 AA; 27709 MW; AI72A4D070E119B7 CRC64;

Query Match 43.0%; Score 40; DB 1; Length 252;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 DSNKTRIDEANQRTATMQL 19
Db 185 DATITNTDEATQALRMV 202

RESULT 12
KINH DROME STANDARD; PRT; 975 AA.
AC P17210; Q9V7L9;
DT 01-AUG-1990 (Rel. 15, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinesin heavy chain.
GN KHC OR KIN OR CG7765.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168428; PubMed=2522352;
RA Yang J.T., Laymon R.A., Goldstein L.S.B.;
RT "A three-domain structure of kinesin heavy chain revealed by DNA
RT sequence and microtubule binding analyses.";
RL Cell 56:879-889(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fogle C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP MUTAGENESIS.
RX MEDLINE=93030741; PubMed=1384131;
RA Cho M., McDonald K., Ganetzky B., Saxton W.M.;
RT "Effects of kinesis mutations on neuronal functions.";
RL Science 258:313-316(1992).
CC -1- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
CC -1- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
CC CHAINS.
CC -1- DOMAIN: Composed of three structural domains: a large globular N-
CC terminal domain which is responsible for the motor activity of
CC kinesin (it hydrolyzes ATP and binds microtubule), a central
CC alpha-helical coiled coil domain that mediates the heavy chain
CC dimerization; and a small globular C-terminal domain which
CC interacts with other proteins (such as the kinesin light chains),
CC vesicles and membranous organelles.
CC -1- MISCELLANEOUS: MUTANT FLIES DISPLAY IMPAIRED ACTION POTENTIAL
CC PROPAGATION AND NEUROTRANSMITTER RELEASE AT NEUROMUSCULAR
CC JUNCTIONS, BUT ARE STILL CAPABLE OF TRANSPORTING CERTAIN
CC MEMBRANES, INCLUDING SYNAPTIC VESICLES, TO THE NERVE TERMINAL.
CC -1- SIMILARITY: Belongs to the kinesin-like protein family. Kinesin
CC subfamily.
CC -----
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CC -----
CC EMBL; M24441; AAA28652.1; -
CC EMBL; AE003807; AAF58029.1; -
CC PIR; A31497; A31497.
CC HSP; P33176; IBG2.
CC Flybase; FBgn0001308; Khc.
CC GO; GO:0005871; C:kinesin complex; IDA.
CC GO; GO:0008017; F:microtubule binding; IDA.
CC GO; GO:0003774; F:motor activity; NAS.
CC GO; GO:0007310; P:occyte dorsal/ventral axis determination; IMP.
CC GO; GO:0007317; P:occyte dorsal/ventral axis determination; IMP.
CC InterPro; IPR001752; kinesin_motor.
CC Pfam; PF00225; kinesin; 1.
CC PRINTS; PR00380; KINESIN.
CC PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
CC PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.

```

KW Motor protein; Microtubule; ATP-binding; Coiled coil.
 FT DOMAIN 1 334 KINESIN-MOTOR (BY SIMILARITY).
 FT DOMAIN 335 931 COILED COIL.
 FT DOMAIN 932 975 GLOBULAR.
 FT DOMAIN 180 321 MICROTUBULE-BINDING.
 FT NP_BIND 92 99 ATP (BY SIMILARITY).
 FT CONFLICT 515 515 A -> T (IN REF. 1).
 SQ SEQUENCE 975 AA; 110399 MW; 24840EF414790888 CRC64;

Query Match 43.0%; Score 40; DB 1; Length 975;
 Best Local Similarity 42.1%; Pred. No. 1e+02;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANORATKML 19
 DB 276 ADGNKTHPYRDSKLTRIL 294

RESULT 13

ARF1_DICDI STANDARD; PRT; 181 AA.
 AC 000909;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE ADP-ribosylation factor 1.
 GN ARF1 OR ARF1.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 CC NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jones D., Morgan C., Insall R., Cockcroft S.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: GTP-binding protein that functions as an allosteric
 CC activator of the cholera toxin catalytic subunit, an ADP-
 CC ribosyltransferase. Involved in protein trafficking; may modulate
 CC vesicle budding and uncoating within the Golgi apparatus (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Arf family.

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 CC -----

DR EMBL; AJ200063; CAA03896.1; -;
 DR HSP; P32889; 1RRP.
 DR Dictybase; DB0001681; arfA.
 DR InterPro; IPR006688; ARF.
 DR InterPro; IPR006689; ARF/SAR.
 DR InterPro; IPR001806; Ras transfrmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00025; arf; 1.
 DR PRINTS; PRO0449; RASTRNSFRMG.
 DR PRINTS; PRO0328; SAR1GTPBP.
 DR SMART; SM00177; ARF; 1.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS01019; ARF; 1
 KW GTP-binding; Myristate; Protein transport; Golgi stack; Lipoprotein.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT LIPID 1 1 N-myristoyl glycine (potential).
 FT NP_BIND 23 30 GTP (BY SIMILARITY).
 FT NP_BIND 66 70 GTP (BY SIMILARITY).
 FT NP_BIND 125 128 GTP (BY SIMILARITY).
 SQ SEQUENCE 181 AA; 20550 MW; 87AE5F2B2F230158 CRC64;

Query Match 42.5%; Score 39.5; DB 1; Length 181;
 Best Local Similarity 57.9%; Pred. No. 19;
 Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 2 DSN-KTRIDEANORATKML 19
 DB 92 DSNDRERIQACDELTKML 110

RESULT 14

CAL2_PASTE STANDARD; PRT; 294 AA.
 ID CAL2_PASTE
 AC Q94715;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative cathepsin L2 (EC 3.4.22.15) (Fragment).
 OS Paramacium tetraurelia.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramacium.
 CC NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Stock 51;
 RX MEDLINE=96248439; PubMed=8665938;
 RA Voelkel H., Kurz U., Linder J., Klumpp S., Gnaul V., Jung G.,
 RA Schultz J.E.;
 RT "Cathepsin L is an intracellular and extracellular protease in
 RT Paramacium tetraurelia: Purification, cloning, sequencing and specific
 RT inhibition by its expressed propeptide."
 RL Eur. J. Biochem. 238:198-206 (1996).
 CC -!- FUNCTION: May be involved in extracellular digestion.
 CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As
 CC compared to cathepsin B, cathepsin L exhibits higher activity
 CC towards protein substrates, but has little activity on Z-Arg-Arg-
 CC NMEc, and no peptidyl-dipeptidase activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to peptidase family C1.
 CC -!- CAUTION: This protein may be non-functional as it lacks the
 CC cysteine active site residue which is replaced by Gly-118.

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 CC -----

DR EMBL; X91756; CAA62871.1; -;
 DR PIR; S68784; S68784.
 DR HSP; O60911; 1FH0.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprot_acsite.
 DR Pfam; PF00112; Peptidase_C1; 1.
 DR ProDom; PD000158; Peptidase_C1; 1.
 DR SMART; SM00645; Pept C1; 1.
 DR PROSITE; PS00640; THIOI_PROTEASE ASN; FALSE NEG.
 DR PROSITE; PS00139; THIOI_PROTEASE CYS; FALSE NEG.
 DR PROSITE; PS00639; THIOI_PROTEASE_HIS; FALSE_NEG.
 KW Hydrolase; Thiol protease.
 FT NON_TER 1 1
 FT PROPEP <1 ? ACTIVATION PEPTIDE.
 FT CHAIN ? 294 PUTATIVE CATHEPSIN L2.
 FT SITE 118 118 POSITION OF ACTIVE SITE CYS.
 FT ACT_SITE 247 247 BY SIMILARITY.
 FT ACT_SITE 264 264 BY SIMILARITY.
 FT DISULFID 115 156 BY SIMILARITY.
 FT DISULFID 240 284 BY SIMILARITY.
 SQ SEQUENCE 294 AA; 33627 MW; 6FD686A0176BEC51 CRC64;

Query Match 41.9%; Score 39; DB 1; Length 294;
 Best Local Similarity 61.5%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DSNKTRIDEANQR 14

```

Db          :||||| |:|||||
            39 NSNKMIEHNQR 51

RESULT 15
MRAW SHEVI
ID MRAW SHEVI STANDARD; PRT; 313 AA.
AC Q9FLN8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-adenosyl-methyltransferase mraw (EC 2.1.1.-).
GN MRAW.
OS Shewanella violacea.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=60217;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSS12;
RA Ishii A., Nakasone K., Sato T., Sugai M., Wachi M., Nagai K., Kato C.;
RT "Isolation and characterization of dcw gene cluster for cell division
RT and cell wall synthesis from a deep-sea piezophilic Shewanella
RT violacea."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase
CC activity (By similarity).
CC -!- SIMILARITY: Belongs to the mraw family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB052554; BAB19194.1; -
DR HAVAP; MF 01007; -; 1
DR InterPro; IPR002903; Bac_Metrnfrse.
DR Pfam; PF01795; Methyltransf_5; 1.
DR ProDom; PD004685; Bac_Metrnfrse; 1.
DR TIGRFAMs; TIGR00006; TIGR00006; 1.
KW Transferase; Methyltransferase.
SQ SEQUENCE 313 AA; 35023 MW; EEF017A946AC43A1 CRC64;

Query Match 41.9%; Score 39; DB 1; Length 313;
Best Local Similarity 52.9%; Pred. NO. 42;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANORATK 17
   : ||||| : |||||
DB 272 AEINKTRLLKAVGKATK 288

Search completed: March 9, 2004, 11:08:10
Job time : 11.7838 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2004, 11:07:42 ; Search time 28.2432 Seconds
(without alignments)
142.049 Million cell updates/sec

Title: US-10-030-485a-6

Perfect score: 93
Sequence: 1 ADSNKTIDEANORATKML 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 93 | 100.0 | 21 | 10 | US-09-942-024-89 |
| 2 | 93 | 100.0 | 21 | 10 | US-09-942-098-89 |
| 3 | 93 | 100.0 | 24 | 10 | US-09-942-024-90 |
| 4 | 93 | 100.0 | 24 | 10 | US-09-942-098-90 |
| 5 | 93 | 100.0 | 33 | 10 | US-09-942-024-33 |
| 6 | 93 | 100.0 | 33 | 10 | US-09-942-024-37 |
| 7 | 93 | 100.0 | 33 | 10 | US-09-942-024-38 |
| 8 | 93 | 100.0 | 33 | 10 | US-09-942-098-33 |
| 9 | 93 | 100.0 | 33 | 10 | US-09-942-098-37 |
| 10 | 93 | 100.0 | 33 | 10 | US-09-942-098-38 |
| 11 | 93 | 100.0 | 116 | 10 | US-09-942-360B-11 |
| 12 | 93 | 100.0 | 203 | 10 | US-09-942-024-14 |
| 13 | 93 | 100.0 | 203 | 10 | US-09-942-024-14 |
| 14 | 93 | 100.0 | 206 | 10 | US-09-942-024-2 |
| 15 | 93 | 100.0 | 206 | 10 | US-09-942-024-7 |

Sequence 12, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 12, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 12, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 2, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 48, Appl
Sequence 52, Appl
Sequence 56, Appl
Sequence 48, Appl

ALIGNMENTS

RESULT 1

US-09-942-024-89
; Sequence 89, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Pect Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: ANIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-89

Query Match 100.08; Score 93; DB 10; Length 21;
Best Local Similarity 100.08; Pred. No. 7.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADSNKTIDEANORATKML 19
|||||

```
Db      2 ADSNKTIDEANQRATKML 20

RESULT 2
US-09-942-098-89
; Sequence 89, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-89

Query Match      100.0%; Score 93; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.9e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||
Db      2 ADSNKTIDEANQRATKML 20
      |||

US-09-942-098-90
; Sequence 90, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-90

Query Match      100.0%; Score 93; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||
Db      2 ADSNKTIDEANQRATKML 20
      |||

US-09-942-024-33
; Sequence 33, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-33

Query Match      100.0%; Score 93; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADSNKTIDEANQRATKML 19
      |||
Db      2 ADSNKTIDEANQRATKML 20
      |||

US-09-942-024-33
; Sequence 33, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-33
```

Query Match 100.0%; Score 93; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTKML 19
 |||||
 Db 12 ADSNKTIDEANQRTKML 30

RESULT 6

US-09-942-024-37
 ; Sequence 37, Application US/09942024
 ; Publication No. US20030143650A1

; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Botulinum
 ; FILE REFERENCE: P-AR 4803
 ; CURRENT FILING DATE: 2001-08-28
 ; CURRENT APPLICATION NUMBER: US/09/942,024
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Carassius auratus

US-09-942-024-37
 ; Sequence 37, Application US/09942024
 ; Publication No. US20030143650A1

Query Match 100.0%; Score 93; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTKML 19
 |||||
 Db 12 ADSNKTIDEANQRTKML 30

RESULT 7

US-09-942-024-38
 ; Sequence 38, Application US/09942024
 ; Publication No. US20030143650A1

; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Botulinum
 ; FILE REFERENCE: P-AR 4803
 ; CURRENT FILING DATE: 2001-08-28
 ; CURRENT APPLICATION NUMBER: US/09/942,024
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Carassius auratus

US-09-942-024-38
 ; Sequence 38, Application US/09942024
 ; Publication No. US20030143650A1

Query Match 100.0%; Score 93; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTKML 19
 |||||
 Db 12 ADSNKTIDEANQRTKML 30

RESULT 8

US-09-942-098-33
 ; Sequence 33, Application US/09942098

; Publication No. US20030143651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Clostridial
 ; FILE REFERENCE: P-AR 4802
 ; CURRENT FILING DATE: 2001-08-28
 ; CURRENT APPLICATION NUMBER: US/09/942,098
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 33
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Mus musculus

US-09-942-098-33

Query Match 100.0%; Score 93; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTKML 19
 |||||
 Db 12 ADSNKTIDEANQRTKML 30

RESULT 9

US-09-942-098-37
 ; Sequence 37, Application US/09942098
 ; Publication No. US20030143651A1

; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Clostridial
 ; FILE REFERENCE: P-AR 4802
 ; CURRENT FILING DATE: 2001-08-28
 ; CURRENT APPLICATION NUMBER: US/09/942,098
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Carassius auratus

US-09-942-098-37

Query Match 100.0%; Score 93; DB 10; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTKML 19
 |||||
 Db 12 ADSNKTIDEANQRTKML 30

RESULT 10

US-09-942-098-38
 ; Sequence 38, Application US/09942098
 ; Publication No. US20030143651A1

; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Clostridial
 ; FILE REFERENCE: P-AR 4802
 ; CURRENT FILING DATE: 2001-08-28
 ; CURRENT APPLICATION NUMBER: US/09/942,098
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38

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; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-38

Query Match      100.0%; Score 93; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 12 ADSNKTTRIDEANQRATKML 30

RESULT 11
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; FILE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11

Query Match      100.0%; Score 93; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 94 ADSNKTTRIDEANQRATKML 112

RESULT 12
US-09-942-024-14
; Sequence 14, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-14

Query Match      100.0%; Score 93; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 182 ADSNKTTRIDEANQRATKML 200

RESULT 13
US-09-942-098-14
; Sequence 14, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-14

Query Match      100.0%; Score 93; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 182 ADSNKTTRIDEANQRATKML 200

RESULT 14
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match      100.0%; Score 93; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 185 ADSNKTTRIDEANQRATKML 203

RESULT 15
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
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; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Pret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match 100.0%; Score 93; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANQRATKML 19
| | | | | | | | | | | | | | | | | | | | | |
Db 185 ADSNKTIDEANQRATKML 203

Search completed: March 9, 2004, 11:12:07
Job time : 28.2432 secs

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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:36 ; Search time 13.8649 Seconds
(without alignments)
131.818 Million cell updates/sec

Title: US-10-030-485A-6
Perfect score: 93
Sequence: 1 ADSNKTREIDANQRTKML 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_78:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 93 | 100.0 | 203 | 2 I50481 | synapse protein SN |
| 2 | 93 | 100.0 | 204 | 2 I50480 | synapse protein SN |
| 3 | 93 | 100.0 | 206 | 2 A37861 | synaptosomal-assoc |
| 4 | 93 | 100.0 | 206 | 2 I53735 | nerve terminal pro |
| 5 | 93 | 100.0 | 206 | 2 I67823 | nerve terminal pro |
| 6 | 93 | 100.0 | 206 | 2 A33623 | synaptosomal-assoc |
| 7 | 70 | 75.3 | 210 | 2 I50552 | synapse protein - |
| 8 | 60 | 64.5 | 210 | 2 JCS512 | SNARE protein 23 - |
| 9 | 56 | 60.2 | 158 | 2 JCS297 | vesicle-membrane f |
| 10 | 56 | 60.2 | 211 | 2 JCS296 | vesicle-membrane f |
| 11 | 48 | 51.6 | 234 | 2 T26553 | hypothetical prote |
| 12 | 46 | 49.5 | 2288 | 2 T29999 | hypothetical prote |
| 13 | 44.5 | 47.8 | 29 | 2 A49708 | synaptosomal-assoc |
| 14 | 44 | 47.3 | 401 | 2 E81436 | transmembrane tran |
| 15 | 44 | 47.3 | 1787 | 2 AG1360 | probable tape-meas |
| 16 | 43 | 46.2 | 1582 | 2 AC1153 | adhesin homolog lm |
| 17 | 42 | 45.2 | 83 | 2 A33854 | outer membrane lip |
| 18 | 42 | 45.2 | 219 | 2 AB1996 | hypothetical prote |
| 19 | 42 | 45.2 | 420 | 2 S50562 | hypothetical prote |
| 20 | 42 | 45.2 | 680 | 2 H70347 | outer membrane pro |
| 21 | 41.5 | 44.6 | 181 | 2 JCA946 | ADP-ribosylation f |
| 22 | 41.5 | 44.6 | 181 | 2 A45422 | ADP-ribosylation f |
| 23 | 41 | 44.1 | 201 | 2 T09047 | hypothetical prote |
| 24 | 41 | 44.1 | 393 | 2 T32127 | hypothetical prote |
| 25 | 41 | 44.1 | 438 | 2 B71963 | probable outer mem |
| 26 | 41 | 44.1 | 494 | 2 S64386 | pre-mRNA splicing |
| 27 | 41 | 44.1 | 575 | 2 F96966 | methyl-accepting c |
| 28 | 41 | 44.1 | 642 | 2 G90551 | lipoprotein (impor |

ALIGNMENTS

RESULT 1

I50481
synapse protein SNAP-25 - goldfish
C/Species: Carassius auratus (goldfish)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C/Accession: I50481
R/Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A/Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A/Reference number: A49632; MUID:94068448; PMID:8248151
A/Accession: I50481
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-203 <RIS>
A/Cross-references: GB:I22976; NID:g349430; PIDN:AAA16538.1; PID:g349431
C/Genetics:
A/Gene: SNAP-25

Query Match 100.0%; Score 93; DB 2; Length 203;

Best Local Similarity 100.0%; Pred. No. 7.6e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTREIDANQRTKML 19
Db 182 ADSNKTREIDANQRTKML 200

RESULT 2

I50480
synapse protein SNAP-25 - goldfish
C/Species: Carassius auratus (goldfish)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C/Accession: I50480
R/Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A/Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A/Reference number: A49632; MUID:94068448; PMID:8248151
A/Accession: I50480
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-204 <RIS>
A/Cross-references: GB:I22973; NID:g349426; PIDN:AAA16537.1; PID:g349427
C/Genetics:
A/Gene: SNAP-25

Query Match 100.0%; Score 93; DB 2; Length 204;

Best Local Similarity 100.0%; Pred. No. 7.6e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTREIDANQRTKML 19
Db 182 ADSNKTREIDANQRTKML 200

30 41 44.1 1578 2 AD1512
31 40.5 43.5 1314 2 T09481
32 40 43.0 243 2 T20653
33 40 43.0 540 2 T34187
34 40 43.0 975 1 A31497
35 40 43.0 1302 1 JC6009
36 39.5 42.5 180 2 T32978
37 39 41.9 71 2 D84748
38 39 41.9 294 2 S68784
39 39 41.9 644 2 D71427
40 39 41.9 664 2 T51247
41 38.5 41.4 200 2 S71036
42 38.5 41.4 918 2 G88545
43 38.5 41.4 943 2 S31132
44 38.5 41.4 1337 2 T30291
45 38 40.9 105 2 E95039

peptidoglycan boun
mating type silenc
hypothetical prote
hypothetical prote
kinesin heavy chai
surface-located me
ADP-ribosylation f
hypothetical prote
cathepsin L - Para
receptor-like prot
ARR2 protein limpo
swarmer initiation
protein F5952.12 f
hypothetical prote
dextranase - Strep
cell division prot

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Query Match      86.0%; Score 80; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNKTRIDEANQRATKML 19
   |||||:|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 13
US-08-743-894B-49
; Sequence 49, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-27

Query Match      84.9%; Score 79; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SNKTRIDEANQRATKML 18
   |||||:|||||
Db 1 SNKTRIDEANQRATKML 16

RESULT 14
US-08-743-894B-27
; Sequence 27, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-30

Query Match      84.9%; Score 79; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SNKTRIDEANQRATKML 19
   |||||:|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 15
US-08-743-894B-30
; Sequence 30, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-27
```

```
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 9
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-30

Query Match      84.9%; Score 79; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 SNKTRIDEANQGRATYML 19
        |||||  |||||
Db      1 SNKTRIDEXNQGRATYML 17

Search completed: March 9, 2004, 11:10:59
Job time : 16.9459 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2004, 10:57:21 ; Search time 52.3784 Seconds
(without alignments)
102.493 Million cell updates/sec

Title: US-10-030-485A-6

Perfect score: 93
Sequence: 1 ADSNKRTRIDANQATYKML 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq.29Jan04.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB | ID | Description |
|------------|-------|---------|-------|--------|----------|-----------|--------------------|
| 1 | 93 | 100.0 | 19 | 4 | AAB15586 | Human SNA | AAB15586 Human SNA |
| 2 | 93 | 100.0 | 21 | 6 | AAB36734 | Fret subs | AAB36734 Fret subs |
| 3 | 93 | 100.0 | 24 | 6 | AAB36735 | Fret subs | AAB36735 Fret subs |
| 4 | 93 | 100.0 | 26 | 2 | AAW30099 | Neurotran | AAW30099 Neurotran |
| 5 | 93 | 100.0 | 33 | 6 | AAB36682 | Goldfish | AAB36682 Goldfish |
| 6 | 93 | 100.0 | 33 | 6 | AAB36683 | Goldfish | AAB36683 Goldfish |
| 7 | 93 | 100.0 | 33 | 6 | AAB36678 | SNAP-25 | AAB36678 SNAP-25 p |
| 8 | 93 | 100.0 | 37 | 2 | AAW30097 | Neurotran | AAW30097 Neurotran |
| 9 | 93 | 100.0 | 70 | 2 | AAW86823 | SNAP-25 r | AAW86823 SNAP-25 r |
| 10 | 93 | 100.0 | 86 | 4 | AAB15584 | Human SNA | AAB15584 Human SNA |
| 11 | 93 | 100.0 | 116 | 5 | AAO15165 | Clostridi | AAO15165 Clostridi |
| 12 | 93 | 100.0 | 206 | 2 | AAW30103 | Synaptoso | AAW30103 Synaptoso |
| 13 | 93 | 100.0 | 206 | 2 | AAW43426 | Mouse syn | AAW43426 Mouse syn |
| 14 | 93 | 100.0 | 206 | 2 | AAW79198 | Mouse SNA | AAW79198 Mouse SNA |
| 15 | 93 | 100.0 | 206 | 4 | AAU00246 | Synaptoso | AAU00246 Synaptoso |
| 16 | 93 | 100.0 | 206 | 4 | AAU00253 | SNARE hom | AAU00253 SNARE hom |
| 17 | 93 | 100.0 | 206 | 4 | AAU00252 | SNARE hom | AAU00252 SNARE hom |
| 18 | 93 | 100.0 | 206 | 6 | AAE36662 | Human SNA | AAE36662 Human SNA |
| 19 | 93 | 100.0 | 206 | 6 | AAE36667 | Rat VAMP- | AAE36667 Rat VAMP- |
| 20 | 93 | 100.0 | 206 | 7 | ADSE4280 | Rat Prote | ADSE4280 Rat Prote |
| 21 | 93 | 100.0 | 206 | 7 | ADSE4288 | Rat Prote | ADSE4288 Rat Prote |
| 22 | 93 | 100.0 | 206 | 7 | ADSE4276 | Rat Prote | ADSE4276 Rat Prote |
| 23 | 93 | 100.0 | 206 | 7 | ADSE4290 | Human Pro | ADSE4290 Human Pro |
| 24 | 93 | 100.0 | 206 | 7 | ADSE4282 | Rat Prote | ADSE4282 Rat Prote |
| 25 | 93 | 100.0 | 206 | 7 | ADSE4274 | Rat Prote | ADSE4274 Rat Prote |

| | | | | | | |
|----|----|-------|-----|---|----------|-----------|
| 26 | 93 | 100.0 | 206 | 7 | ADSE4286 | Human Pro |
| 27 | 93 | 100.0 | 206 | 7 | ADSE4284 | Rat Prote |
| 28 | 93 | 100.0 | 206 | 7 | ADSE4272 | Rat Prote |
| 29 | 93 | 100.0 | 206 | 7 | ADSE4278 | Rat Prote |
| 30 | 89 | 95.7 | 18 | 6 | AAE36677 | Human SNA |
| 31 | 89 | 95.7 | 23 | 6 | AAE36733 | Fret subs |
| 32 | 89 | 95.7 | 206 | 4 | AAU02640 | Synaptoso |
| 33 | 87 | 93.5 | 116 | 5 | AAO15166 | Clostridi |
| 34 | 87 | 93.5 | 203 | 4 | AAU02636 | Synaptoso |
| 35 | 87 | 93.5 | 206 | 4 | AAU00261 | Synaptoso |
| 36 | 87 | 93.5 | 206 | 4 | AAU00259 | Synaptoso |
| 37 | 87 | 93.5 | 206 | 4 | AAU00260 | Synaptoso |
| 38 | 87 | 93.5 | 206 | 4 | AAU02638 | Synaptoso |
| 39 | 86 | 92.5 | 206 | 4 | AAU00262 | Synaptoso |
| 40 | 85 | 91.4 | 17 | 6 | AAE36676 | Human SNA |
| 41 | 84 | 90.3 | 206 | 4 | AAU00266 | Synaptoso |
| 42 | 84 | 90.3 | 206 | 4 | AAU00257 | Synaptoso |
| 43 | 83 | 89.2 | 17 | 2 | AAV44057 | Human SNA |
| 44 | 83 | 89.2 | 17 | 2 | AAV44021 | Amino aci |
| 45 | 83 | 89.2 | 17 | 5 | ABG69065 | Human pol |

ALIGNMENTS

RESULT 1

AAB15586
ID AAB15586 standard; peptide; 19 AA.

XX AAB15586;

XX DT 02-MAR-2001 (first entry)

XX DE Human SNAP-25 N-terminal peptide #6.

XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.

XX OS Homo sapiens.

XX PN WO200064932-A1.

XX PD 02-NOV-2000.

XX PF 18-FEB-2000; 2000WO-ES0000058.

XX PR 23-APR-1999; 99ES-00000844.

XX PA (LIPO-) LIPOTEC SA.

XX PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;

XX DR WPI; 2001-007091/01.

XX PT New peptides containing amino acid sequences from known proteins for
treatment of neurological disorders.

XX PS Claim 17; Page 34; 40pp; Spanish.

XX CC The invention relates to new peptides comprising 3-30 contiguous amino
acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
protein 25). The peptides AAB15581-B15586 represent examples of the
peptides of the invention. The peptides have neuronal exocytosis
inhibitory activity and are used for treatment of facial wrinkles and
asymmetry and pathological neuronal exocytosis-mediated pathological
disorders and alterations manifested e.g. by spasms and neurological and
neurodegenerative disorders

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 93; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTATKML 19
 DB 1 ADSNKTIDEANQRTATKML 19

RESULT 2
 AAE36734
 ID AAE36734 standard; peptide; 21 AA.
 AC AAE36734;
 DT 07-AUG-2003 (first entry)
 DE Fret substrate peptide #5 used in the invention.
 XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX Unidentified.
 OS

Key Location/Qualifiers
 FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
 FT given as Xaa in the sequence shown as SEQ ID NO: 89 in
 FT the sequence listing of the specification"
 FT 21
 FT Modified-site 21 /note= "Tetramethylrhodamine-modified Lysine; C-terminal
 FT amide; This residue is given as Xaa in the sequence shown
 FT as SEQ ID NO: 89 in the sequence listing of the
 FT specification"
 XX WO2003020948-A2.
 PN
 XX
 XX 13-MAR-2003.
 PD
 XX
 XX 22-AUG-2002; 2002WO-US027145.
 PF
 XX
 XX 28-AUG-2001; 2001US-00942024.
 PR
 XX
 XX (ALLR) ALLERGAN INC.
 PA
 XX
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX
 XX WPI; 2003-290198/28.
 DR
 XX
 XX Example 1; Page 115; 168pp; English.

Botulinum serotype A/E substrate useful for assaying protease activity of
 botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 toxin recognition sequence that includes a cleavage site.

The present invention relates to novel clostridium toxin substrates. The
 invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 which comprise a donor fluorophore, an acceptor having an absorbance
 spectrum overlapping the emission spectrum of the donor fluorophore and a
 BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 the cleavage site intervenes between the donor fluorophore and acceptor
 and under the appropriate conditions, the resonance energy transfer is
 exhibited between the donor and acceptor. Natural targets of clostridium
 neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 of the invention are useful in assaying for the protease activity of a
 sample from a human or animal, for
 e.g., exposed to clostridial toxin or having one or more symptoms of a

CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ Sequence 21 AA;
 Query Match 100.0%; Score 93; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.4e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRTATKML 19
 DB 2 ADSNKTIDEANQRTATKML 20

RESULT 3
 AAE36735
 ID AAE36735 standard; peptide; 24 AA.
 AC AAE36735;
 DT 07-AUG-2003 (first entry)
 DE Fret substrate peptide #6 used in the invention.
 XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX Unidentified.
 OS

Key Location/Qualifiers
 FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
 FT given as Xaa in the sequence shown as SEQ ID NO: 90 in
 FT the sequence listing of the specification"
 FT 24
 FT Modified-site 24 /note= "Tetramethylrhodamine-modified Lysine; C-terminal
 FT amide; This residue is given as Xaa in the sequence shown
 FT as SEQ ID NO: 90 in the sequence listing of the
 FT specification"
 XX WO2003020948-A2.
 PN
 XX
 XX 13-MAR-2003.
 PD
 XX
 XX 22-AUG-2002; 2002WO-US027145.
 PF
 XX
 XX 28-AUG-2001; 2001US-00942024.
 PR
 XX
 XX (ALLR) ALLERGAN INC.
 PA
 XX
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX
 XX WPI; 2003-290198/28.
 DR
 XX
 XX Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX
 XX Example 1; Page 115; 168pp; English.

The present invention relates to novel clostridium toxin substrates. The
 invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 which comprise a donor fluorophore, an acceptor having an absorbance
 spectrum overlapping the emission spectrum of the donor fluorophore and a
 BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 the cleavage site intervenes between the donor fluorophore and acceptor
 and under the appropriate conditions, the resonance energy transfer is
 exhibited between the donor and acceptor. Natural targets of clostridium
 neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 of the invention are useful in assaying for the protease activity of any
 clostridial toxin including botulinum toxins of all serotypes and tetanus
 toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 lysate, raw, cooked or processed foods, beverages, animal feed, soil
 samples, water samples, cosmetics, tissue samples and beverage or food
 samples. They are useful to assay a sample from a human or animal, for
 e.g., exposed to clostridial toxin or having one or more symptoms of a

CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention

XX Sequence 24 AA;

Query Match 100.0%; Score 93; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANORATKML 19
 Db 2 ADSNKTIDEANORATKML 20

RESULT 4
 AAW30099
 ID AAW30099 standard; peptide; 26 AA.

XX AAW30099;

XX 06-APR-1998 (first entry)

XX Neurotransmitter secretion inhibitor #3.

XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 XX excitation-secretory uncoupling peptide; catecholamine secretion;
 XX bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 XX synaptosomal associated protein; SNAP-25.

XX Homo sapiens.

XX WO9734620-A1.

XX 25-SEP-1997.

XX 18-MAR-1997; 97WO-US004393.

XX 18-MAR-1996; 96US-0013599P.

XX (REGC) UNIV CALIFORNIA.

XX Montal M;

XX WPI; 1997-479986/44.

XX Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.

XX Claim 13; Page 31; 61pp; English.

XX This sequence corresponds to residues 181-206 of the human 25 kD
 CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of
 CC the invention. The agents of the invention inhibit secretion of
 CC neurotransmitter from neuronal cells and is an excitation-secretory
 CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
 CC correspond substantially to any one of AAW30097-W30102, or more generally
 CC any (I) that inhibits 50% of catecholamine secretion from bovine
 CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
 CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
 CC release of neurotransmitters from synaptic vesicles, specifically for
 CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
 CC imaging of intracellular distribution of (I). Compounds for delivering
 CC the drug to neural cells provide targeted drug delivery, e.g. of
 CC substance P to brain tumours for induction of apoptosis. Unlike the

CC neurotoxins, (I) are not toxic or immunogenic and are more readily
 CC available. Their therapeutic effect lasts for several days or weeks, so
 CC lower doses or less frequent treatments are required

XX Sequence 26 AA;

Query Match 100.0%; Score 93; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADSNKTIDEANORATKML 19
 Db 5 ADSNKTIDEANORATKML 23

RESULT 5
 AAE36682
 ID AAE36682 standard; peptide; 33 AA.

XX AAE36682;

XX 07-AUG-2003 (first entry)

XX Goldfish SNAP-25A peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;
 XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 XX TeNT; cosmetic.

XX Carassius auratus.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"

FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"

FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food

CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish
 CC SNAP-25A peptide used in the invention
 XX

SQ Sequence 33 AA;

Query Match 100.0%; Score 93; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKRTRIDEANQRATKML 19
 |||||
 DB 12 ADSNKRTRIDEANQRATKML 30

RESULT 6

AAE36683
 ID AAE36683 standard; peptide; 33 AA.

XX AAE36683;

DT 07-AUG-2003 (first entry)

XX Goldfish SNAP-25B peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW TeNT; cosmetic.

XX Carassius auratus.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"

FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"

FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of

PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial

PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The

CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates

CC which comprise a donor fluorophore, an acceptor having an absorbance

CC spectrum overlapping the emission spectrum of the donor fluorophore and a

CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where

CC the cleavage site intervenes between the donor fluorophore and acceptor

CC and under the appropriate conditions, the resonance energy transfer is

CC exhibited between the donor and acceptor. Natural targets of clostridium

CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences

CC of the invention are useful in assaying for the protease activity of any

CC clostridial toxin including botulinum toxins of all serotypes and tetanus

CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish
 CC SNAP-25B peptide used in the invention
 XX

SQ Sequence 33 AA;

Query Match 100.0%; Score 93; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. No. 4e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKRTRIDEANQRATKML 19

|||||

DB 12 ADSNKRTRIDEANQRATKML 30

RESULT 7

AAE36678

ID AAE36678 standard; peptide; 33 AA.

XX AAE36678;

DT 07-AUG-2003 (first entry)

XX SNAP-25 peptide.

XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;

KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

KW cosmetic; mouse; rat.

XX Homo sapiens.

OS Mus musculus.

OS Rattus sp.

XX Key Location/Qualifiers

FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"

FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"

FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of

PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial

PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The

CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates

CC which comprise a donor fluorophore, an acceptor having an absorbance

CC spectrum overlapping the emission spectrum of the donor fluorophore and a

CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where

CC the cleavage site intervenes between the donor fluorophore and acceptor

CC and under the appropriate conditions, the resonance energy transfer is

CC exhibited between the donor and acceptor. Natural targets of clostridium

CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences

CC of the invention are useful in assaying for the protease activity of any

CC clostridial toxin including botulinum toxins of all serotypes and tetanus

CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TENT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25
 CC peptide used in the invention

XX SQ Sequence 33 AA;

Query Match 100.0%; Score 93; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. No. 4e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRATKML 19

DB 12 ADSNKTIDEANQRATKML 30

RESULT 8

AAW30097

ID AAW30097 standard; peptide; 37 AA.

XX AC AAW30097;

XX DT 06-APR-1998 (first entry)

XX DE Neurotransmitter secretion inhibitor #1.

XX KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;

XX KW excitation-secretory uncoupling peptide; catecholamine secretion;

XX KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;

XX KW synaptosomal associated protein; SNAP-25.

XX OS Homo sapiens.

XX PN WO9734620-A1.

XX XX 25-SEP-1997.

XX PF 18-MAR-1997; 97WO-US004393.

XX PR 18-MAR-1996; 96US-0013599P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Montal M;

XX DR WPI; 1997-479986/44.

XX XX Excitation-secretory uncoupling peptide(s) for inhibiting

PT neuro:transmitter release - used particularly for treating muscle

PT spasticity, and for delivering drugs specifically to neural cells.

XX PS Claim 1; Page 30; 61pp; English.

XX XX This sequence corresponds to residues 170-206 of the human 25 kD

CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of

CC the invention. The agents of the invention inhibit secretion of

CC neurotransmitter from neuronal cells and is an excitation-secretory

CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which

CC correspond substantially to any one of AAW30097-W30102, or more generally

CC any (I) that inhibits 50% of catecholamine secretion from bovine

CC chromaffin cells at a concentration of 10 microM, especially 0.25 microM,

CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit

CC release of neurotransmitters from synaptic vesicles, specifically for

CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
 CC imaging of intracellular distribution of (I). Compounds for delivering
 CC the drug to neural cells provide targeted drug delivery, e.g. of
 CC substance P to brain tumours for induction of apoptosis. Unlike the
 CC neurotoxins, (I) are not toxic or immunogenic and are more readily
 CC available. Their therapeutic effect lasts for several days or weeks, so
 CC lower doses or less frequent treatments are required

XX SQ Sequence 37 AA;

Query Match 100.0%; Score 93; DB 2; Length 37;

Best Local Similarity 100.0%; Pred. No. 4.5e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRATKML 19

DB 16 ADSNKTIDEANQRATKML 34

RESULT 9

AAW86823

ID AAW86823 standard; peptide; 70 AA.

XX AC AAW86823;

XX DT 15-AUG-1996 (first entry)

XX DE SNAP-25 residues 137-206.

XX KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;

XX KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;

XX KW antibody; detection; assay.

XX OS Synthetic.

XX PN WO9533850-A1.

XX PD 14-DEC-1995.

XX PF 02-JUN-1995; 95WO-GB001279.

XX PR 03-JUN-1994; 94GB-00011138.

XX PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.

XX PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.

XX PI Shone CC, Hallis B, James BAF, Quinn CP;

XX DR WPI; 1996-040249/04.

XX PT Assay for botulinum or tetanus toxin - by combining test cpd. with

PT substrate which is cleaved by the toxin, and antibody specific for the

PT cleaved but not uncleaved substrate.

XX PS Example 4; Page 19; 48pp; English.

XX XX The botulinum neurotoxins possess highly specific zinc-endopeptidase

CC activities within their light sub-units. Depending on the neurotoxin type

CC these act to cleave small proteins within the nerve cell which are

CC involved in neurotransmitter release. Antibodies are used in assays which

CC detect cleaved but not uncleaved substrate. Assays for botulinum types A

CC and E use the present sequence as a substrate. The sequence is SNAP-25

CC protein, residues 137-206

XX SQ Sequence 70 AA;

Query Match 100.0%; Score 93; DB 2; Length 70;

Best Local Similarity 100.0%; Pred. No. 9.3e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTIDEANQRATKML 19

DB 49 ADSNKTIDEANQRATKML 67

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RESULT 10
AAB15584
ID AAB15584 standard; peptide; 86 AA.
XX
AC AAB15584;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #4.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
PA (LIPO-) LIPOTEC SA.
XX
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX
DR WPI; 2001-007091/01.
XX
PT New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.
XX
PS Claim 16; Page 32-33; 40pp; Spanish.
XX
CC The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders
XX
SQ Sequence 86 AA;
Query Match 100.0%; Score 93; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 65 ADSNKTTRIDEANQRATKML 83
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

RESULT 11
AAO15165
ID AAO15165 standard; peptide; 116 AA.
XX
AC AAO15165;
XX
DT 02-SEP-2002 (first entry)
XX
DE Clostridial neurotoxin protease substrate peptide 4.
XX
KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.
XX
OS Homo sapiens.
XX
PN WO9734620-A1.

XX OS Unidentified.
XX FH Key
XX FT Modified-site 1
XX FT Location/Qualifiers
XX FT /note= "S-fluoresceinyl-cysteine"
XX FT Cleavage-site 89..90
XX FT /note= "The peptide is cleaved between these two residues
XX FT by type E Clostridium botulinum neurotoxin"
XX FT Cleavage-site 106..107
XX FT /note= "The peptide is cleaved between these two residues
XX FT by type A Clostridium botulinum neurotoxin"
XX
XX WO200225284-A2.
XX
XX 28-MAR-2002.
XX
XX 25-SEP-2001; 2001WO-US030188.
XX
XX 25-SEP-2000; 2000US-0235050P.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Schmidt JJ, Stafford RG;
XX
XX WPI; 2002-499829/53.
XX
XX Substrate useful in e.g. an assay for the protease activity of
XX clostridial neurotoxin, comprises modified peptide or protein.
XX
XX Claim 22; Page 16; 48pp; English.
XX
XX The invention comprises clostridial neurotoxin substrate peptides which
XX can serve as fluorescence resonant energy transfer assay (FRET) or
XX quenched-signal substrates in assays for the proteolytic activities of
XX clostridial neurotoxins. The invention further comprises Clostridium
XX botulinum neurotoxin substrate peptides that can serve as immobilised
XX substrates (i.e. bound to a solid phase) in assays for the proteolytic
XX activities of clostridial neurotoxins. The clostridial (including the
XX Clostridium botulinum) neurotoxin substrate peptides are useful for
XX detecting the presence of clostridial neurotoxins in a sample (e.g. food
XX or an environmental sample). The present amino acid sequence represents a
XX clostridial neurotoxin substrate peptide of the invention
XX
XX Sequence 116 AA;
Query Match 100.0%; Score 93; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADSNKTTRIDEANQRATKML 19
Db 94 ADSNKTTRIDEANQRATKML 112
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

RESULT 12
AAW30103
ID AAW30103 standard; peptide; 206 AA.
XX
AC AAW30103;
XX
DT 06-APR-1998 (first entry)
XX
DE Synaptosomal associated protein.
XX
KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
KW excitation-secretory uncoupling peptide; catecholamine secretion;
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW synaptosomal associated protein; SNAP-25.
XX
XX Homo sapiens.
XX
XX WO9734620-A1.

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XX PD 25-SEP-1997.
XX PF 18-MAR-1997; 97WO-US004393.
XX PR 18-MAR-1996; 96US-0013599P.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Montal M;
XX PI WPI; 1997-479986/44.
XX DR
XX DR
XX PT Excitation-secretory uncoupling peptide(s) for inhibiting
XX PT neurotransmitter release - used particularly for treating muscle
XX PT spasticity, and for delivering drugs specifically to neural cells.
XX PS
XX PS Disclosure; Page 27-28; 61pp; English.
XX CC
XX CC This sequence represents the human 25 kD synaptosomal associated protein
XX CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
XX CC the invention inhibit secretion of neurotransmitter from neuronal cells
XX CC and is an excitation-secretory uncoupling peptide (I) of at least 20
XX CC amino acids (aa) all of which correspond substantially to any one of
XX CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
XX CC catecholamine secretion from bovine chromaffin cells at a concentration
XX CC of 10 microm, especially 0.25 microm, or less. (I) are used, as a
XX CC replacement for Clostridium toxin, to inhibit release of
XX CC neurotransmitters from synaptic vesicles, specifically for reducing
XX CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
XX CC intracellular distribution of (I). Compounds for delivering the drug to
XX CC neural cells provide targeted drug delivery, e.g. of substance P to brain
XX CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
XX CC toxic or immunogenic and are more readily available. Their therapeutic
XX CC effect lasts for several days or weeks, so lower doses or less frequent
XX CC treatments are required
XX CC
XX CC Sequence 206 AA;
XX CC
XX CC Query Match 100.0%; Score 93; DB 2; Length 206;
XX CC Best Local Similarity 100.0%; Pred. No. 3.2e-07;
XX CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 1 ADSNKRTRIDEANQRATKML 19
XX CC |||||
XX CC DB 185 ADSNKRTRIDEANQRATKML 203
XX CC
XX CC RESULT 14
XX CC AAW79198
XX CC ID AAW79198 standard; protein; 206 AA.
XX CC AC AAW79198;
XX CC XX
XX CC DT 25-NOV-1998 (first entry)
XX CC XX
XX CC DE Mouse SNAP-25 polypeptide.
XX CC XX
XX CC KW Hrs-2 polypeptide; ATP-prefering nucleotidase; SNAP-25; vesicle docking;
XX CC KW calcium-regulated secretion; secretory vesicle; secretory process; brain;
XX CC KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;
XX CC KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;
XX CC KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;
XX CC KW immune system; antigen processing; immunomodulator; viral processing;
XX CC KW central nervous system; vesicular release; affective disorder; human;
XX CC KW anti-tumour application; membrane trafficking regulation; mouse.
XX CC XX
XX CC OS Mus sp.
XX CC XX
XX CC PN WO9838210-A2.
XX CC XX
XX CC PD 03-SEP-1998.
XX CC XX
XX CC PF 26-FEB-1998; 98WO-US003789.
XX CC XX
XX CC PR 26-FEB-1997; 97US-0039159P.
XX CC XX
XX CC PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX CC XX
XX CC PI Bean AJ, Scheller RH;
XX CC XX
XX CC DR WPI; 1998-481140/41.
XX CC DR N-PSDB; AAV57558.
XX CC XX
XX CC PT New isolated Hrs-2 nucleotidase - used in assays to identify compounds
XX CC PT capable of modulating calcium-regulatory secretion of secretory vesicles,

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PT such as in neurotransmitter release.
 XX Claim 16; Page 42-44; 55pp; English.
 XX This represents a mouse SNAP-25 polypeptide, a component of the protein
 CC polypeptides thought to underlie vesicle docking and fusion. The
 CC invention provides rat and human Hrs-2 polypeptides which are ATP-
 CC preferring nucleotidase that associate with SNAP-25. For identifying a
 CC compound capable of modulating calcium-regulated secretion of secretory
 CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2
 CC polypeptide, in the presence and absence of a test compound. The effect
 CC of the test compound on the extent of binding between the SNAP-25 and Hrs
 CC -2 polypeptides are measured and a compound is identified as effective if
 CC its measured effect on the extent of binding is above a threshold level.
 CC The products can be used for identifying drugs capable of affecting
 CC secretory processes, such as neurotransmitter release at the active zones
 CC of presynaptic membranes. Such drugs can be used for treating disorders
 CC or conditions of the central nervous system by selectively enhancing or
 CC inhibiting vesicular release in specific areas of the brain, including
 CC affective disorders (e.g. depression), disorders of thought (e.g.
 CC schizophrenia) and degenerative disorders (Parkinson's disease), as well
 CC as applications such as anaesthesia. The drugs can also be used
 CC therapeutically in other systems such as the endocrine system for
 CC treatment of hormonal imbalances, the immune system for intervention in
 CC antigen processing, secreted immunomodulators, and viral processing, as
 CC well as anti-tumour applications, such as regulation of membrane
 CC trafficking during rapid cell division
 XX Sequence 206 AA;

Query Match 100.0%; Score 93; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSNKTTRIDEANQRATKML 19
 |||||
 Db 185 ADSNKTTRIDEANQRATKML 203

RESULT 15
 AAU00246
 ID AAU00246 standard; protein; 206 AA.

XX AAU00246;
 XX 12-SEP-2001 (first entry)
 DE Synaptosomal-associated protein, SNAP25.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mutagenic; PCR primer; mouse;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.

XX Key Location/Qualifiers
 FH Cleavage-site 180..181
 FT /note= "Peptide bond susceptible to cleavage by
 FT clostridial neurotoxin"
 FT Cleavage-site 197..198
 FT /note= "Peptide bonds susceptible to cleavage by
 FT clostridial neurotoxin"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 DR Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Disclosure; Fig 8; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25. The sequence was used to create SNAP-25
 CC double/single point mutants and C-terminal deletion mutants used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)- attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state

XX Sequence 206 AA;

Query Match 100.0%; Score 93; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADSNKTTRIDEANQRATKML 19
 |||||
 Db 185 ADSNKTTRIDEANQRATKML 203

Search completed: March 9, 2004, 11:07:36
 Job time : 52.3784 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 10:58:06 ; Search time 10.2162 Seconds
(without alignments)
91.743 Million cell updates/sec

Title: US-10-030-485A-5

Perfect score: 89
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 89 | 100.0 | 204 | 1 SN2A_CARAU | P36977 carassius a |
| 2 | 89 | 100.0 | 206 | 1 SN25_HUMAN | P13795 homo sapien |
| 3 | 80 | 89.9 | 203 | 1 SN2B_CARAU | P36978 carassius a |
| 4 | 60 | 67.4 | 210 | 1 SN25_TORMA | P36976 torpedo mar |
| 5 | 55 | 61.8 | 211 | 1 SN23_HUMAN | O00161 homo sapien |
| 6 | 45 | 50.6 | 212 | 1 SN25_DROME | P36975 drosophila |
| 7 | 43 | 48.3 | 1353 | 1 CVA9_HUMAN | O60503 homo sapien |
| 8 | 41 | 46.1 | 298 | 1 HCD1_CAEEL | P34439 caenorhabdi |
| 9 | 41 | 46.1 | 377 | 1 Y392_CHLTR | P36427 chlamydia t |
| 10 | 41 | 46.1 | 437 | 1 YSH8_CAEEL | O09949 caenorhabdi |
| 11 | 40 | 44.9 | 320 | 1 MCH_WETTH | O26867 methanobact |
| 12 | 40 | 44.9 | 442 | 1 BNB_DROME | P29746 drosophila |
| 13 | 40 | 44.9 | 499 | 1 GAB_LYNGT | P26714 lymaea sta |
| 14 | 40 | 44.9 | 550 | 1 DBP2_SCHPO | P24782 schizosacch |
| 15 | 40 | 44.9 | 580 | 1 SNTD_BOOMI | P52307 boophilus m |
| 16 | 40 | 44.9 | 2867 | 1 RBP2_PLAVB | O00799 plasmodium |
| 17 | 39.5 | 44.4 | 668 | 1 VNC5_FPV19 | P24842 feline panl |
| 18 | 39.5 | 44.4 | 668 | 1 VNC5_PAVCN | P12929 canine parv |
| 19 | 39 | 43.8 | 267 | 1 MLF1_MOUSE | O9QWV4 mus musculu |
| 20 | 39 | 43.8 | 277 | 1 URED_RHIME | P42888 rhizobium m |
| 21 | 39 | 43.8 | 294 | 1 CAL2_PARTE | O94715 paramecium |
| 22 | 39 | 43.8 | 605 | 1 GOX_TALFL | O82452 talaromyces |
| 23 | 39 | 43.8 | 1798 | 1 LMB2_HUMAN | P55268 homo sapien |
| 24 | 39 | 43.8 | 1799 | 1 LMB2_MOUSE | O61292 mus musculu |
| 25 | 39 | 43.8 | 1801 | 1 LMB2_RAT | P15800 rattus norv |
| 26 | 39 | 43.8 | 2164 | 1 POLG_HRV89 | P07210 h genome po |
| 27 | 39 | 43.8 | 3255 | 1 POLG_LMYO | P31999 l genome po |
| 28 | 39 | 43.8 | 3255 | 1 POLG_LMYE | P89876 l genome po |
| 29 | 39 | 43.8 | 7389 | 1 BRA1_MOUSE | O91ZU6 mus musculu |
| 30 | 38.5 | 43.3 | 621 | 1 RFA1_YEAST | P22336 saccharomyc |
| 31 | 38.5 | 43.3 | 640 | 1 DNK1_PORGI | O9ZAD3 porphyromon |
| 32 | 38 | 42.7 | 133 | 1 ATPE_CVACA | O9TM40 cyanidium c |
| 33 | 38 | 42.7 | 184 | 1 ARF2_SCHPO | O9Y722 schizosacch |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 38 | 42.7 | 204 | 1 IPP2_RAT | P50411 rattus norv |
| 35 | 38 | 42.7 | 243 | 1 GTT2_HUMAN | P30712 homo sapien |
| 36 | 38 | 42.7 | 328 | 1 PTA_CLOTS | Q59330 clostridium |
| 37 | 38 | 42.7 | 484 | 1 PAP2_XENLA | P51005 xenopus lae |
| 38 | 38 | 42.7 | 502 | 1 C72A_ARATH | Q91VD2 arabidopsis |
| 39 | 38 | 42.7 | 513 | 1 FLAB_HELPV | Q9ZMW8 helicobacte |
| 40 | 38 | 42.7 | 513 | 1 FLAB_HELPV | Q07911 helicobacte |
| 41 | 38 | 42.7 | 587 | 1 GOX_PENAG | P81156 penicillium |
| 42 | 38 | 42.7 | 704 | 1 MID2_SCHPO | Q9P7Y8 schizosacch |
| 43 | 38 | 42.7 | 785 | 1 YG51_YEAST | P50089 saccharomyc |
| 44 | 38 | 42.7 | 3163 | 1 POLG_TUMVQ | Q02597 t genome po |
| 45 | 38 | 42.7 | 3164 | 1 POLG_TUMVQ | P89509 t genome po |

ALIGNMENTS

```

RESULT 1
SN2A_CARAU STANDARD; PRT; 204 AA.
ID SN2A_CARAU
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptoosomal-associated protein 25A (SNAP-25A).
GN SNAP-A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Retina;
RX MEDLINE=9406848; PubMed=8248151;
RA Risinger C., Larhammer D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish.";
RC Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L22973; AAA16537.1; --
CC F1R; I50480; I50480.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNAP-25; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS0192; T-SNARE; 2.
CC Synaptoosome; Neurone; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CVS-RICH
FT SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;
Query Match 100.0%; Score 89; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 R1MEXADSNKTRIDEANO 18
 DB 178 R1MEXADSNKTRIDEANO 195

RESULT 2
 SN25_HUMAN STANDARD; PRT; 206 AA.
 AC P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
 GN SNAP25 OR SNAP.

OS Homo sapiens (Human).
 OS Macaca mulatta (Rhesus macaque).
 OS Mus musculus (Mouse).
 OS Rattus norvegicus (Rat), and
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606, 9544, 10090, 10116, 9031;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94156217; PubMed=8112622;
 RA Bark I.C., Wilson M.C.;
 RT "Human cDNA clones encoding two different isoforms of the nerve
 terminal protein SNAP-25.";
 RL Gene 139:291-292 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94333829; PubMed=8056350;
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
 RT "Cloning and sequence analysis of the human SNAP25 cDNA.";
 RL Gene 145:313-314 (1994).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Human; TISSUE=Skeletal muscle;
 RX MEDLINE=96332494; PubMed=8760387;
 RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,
 RA Frenkel M.J., Ward C.W.;
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25
 (synaptosomal-associated protein 25) A and B isoforms in addition to
 syntaxin 4 and synaptobrevin 1 and 2.";
 RL Biochem. J. 317:945-954 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Jekosch K., Johnson C.M., Johnson D.,
 RA Leinvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McKay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Selra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Human; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mollaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; TISSUE=Hippocampus;
 RJ Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=BALE/c;
 RX MEDLINE=90078337; PubMed=2592413;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein,
 SNAP-25, differentially expressed by neuronal subpopulations.";
 RL J. Cell Biol. 109:3039-3052 (1989).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=ILS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 within alcohol-related QTLs.";
 RL Mamm. Genome 12:657-663 (2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Mouse; STRAIN=CS7BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354693; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
 RA Strausberg R.L.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Cat;
 RA Kataoka M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Cat; TISSUE=Brain;
 RA Cho A.R., You K.H.;
 RL "Cloning of the SNAP-25 gene from a rat brain cDNA library.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Cat; TISSUE=Brain;
 RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
 RT "SNARE complex proteins, including the cognate pair VAMP-2 and
 RT syntaxin-4, are expressed in cultured oligodendrocytes.";
 RL J. Neurochem. 72:988-998(1999).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; TISSUE=Retina;
 RA MEDLINE=91126080; PubMed=192470;
 RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
 RA Wilson M.C.;
 RT "Expression of a conserved cell-type-specific protein in nerve
 RT terminals coincides with synaptogenesis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
 RN [15]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Chicken;
 RA MEDLINE=93389736; PubMed=8377193;
 RA Bark I.C.;
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
 RT encoding distinct isoforms of the protein.";
 RL J. Mol. Biol. 233:67-76(1993).
 RN [16]
 RP PALMITOYLATION.
 RC SPECIES=Cat;
 RA MEDLINE=93100552; PubMed=1281490;
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
 RT methionine-rich polypeptide in rapid axonal transport and a major

Query Match 100.0%; Score 89; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 DB 180 RIMEKADSNKTRIDEANQ 197
 |||:|||||

RESULT 3
 SN2B_CARAU

ID SN2B_CARAU STANDARD; PRT; 203 AA.
 AC P36976;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25B (SNAP-25B).
 GN SNAP-B.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94068448; PubMed=8248151;
 RA Rislinger C., Larhammar D.;
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
 RT goldfish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 CC specific neuronal systems. Associates with proteins involved in
 CC vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 CC the nerve terminal.
 CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus,
 CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
 CC granule cells of the cerebellum.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC -----
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 CC -----
 CC EMBL; L22976; AAA16538.1;
 DR PIR; I50481; I50481.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; t-SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS0192; t-SNARE; 2.
 KW Synaptosome, Neurone; Repeat; Coiled coil; Multigene family.
 FT DOMAIN 19 81 t-SNARE COILED-COIL HOMOMOLOGY 1.
 FT DOMAIN 137 199 t-SNARE COILED-COIL HOMOMOLOGY 2.
 FT DOMAIN 85 92 CYS-RICH.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBED37D6D7 CRC64;
 Query Match 89.9%; Score 80; DB 1; Length 203;
 Best Local Similarity 88.9%; Pred. No. 1.2e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 DB 177 RIMEKADSNKTRIDEANQ 194
 |||:|||||

RESULT 4
 SN25_TORMA STANDARD; PRT; 210 AA.
 AC P36976;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25).
 OS Torpedo marmorata (Marbled electric ray).

J. Biol. Chem. 271:13300-13303(1996).

[2]

SEQUENCE FROM N.A. (ISOFORMS SNAP-23A AND SNAP-23B).
TISSUE=Neutrophils;
MEDLINE=97224437; PubMed=9070898;
Mollinedo F., Lazo P.A.;
Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 in human neutrophils and HL-60 cells.;
Biochem. Biophys. Res. Commun. 231:808-812(1997).
[3]

SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
Nadal M., Area E., Mollinedo F., Estivill X., Lazo P.A.;
"Exon organization and chromosomal localization of human synaptosomal associated protein-23 (SNAP-23) gene and generation of isoforms by alternative splicing.";
Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[4]

SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
TISSUE=Cervix, Placenta, and Testis;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Boak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E.,
Butcher A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: ESSENTIAL COMPONENT OF THE HIGH AFFINITY RECEPTOR FOR THE GENERAL MEMBRANE FUSION MACHINERY AND AN IMPORTANT REGULATOR OF TRANSPORT VESICLE DOCKING AND FUSION.

-1- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND SYNAPTOBREVINS/VAMPs.

-1- SUBCELLULAR LOCATION: MAINLY LOCALIZED TO THE PLASMA MEMBRANE.

-1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=SNAP-23a;
IsoId=000161-1; Sequence=Displayed;
Name=SNAP-23b;
IsoId=000161-2; Sequence=VSP 006187, VSP 006188;

-1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS WHERE FOUND IN PLACENTA.

-1- SIMILARITY: Belongs to the SNAP-25 family.

-1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

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EMBL; U55936; AAC50537.1; --
EMBL; Y09567; CAAT0760.1; --
EMBL; Y09568; CAAT0761.1; --
EMBL; A011945; CAA09864.1; --
EMBL; BC000148; AAH00148.1; --
EMBL; BC003686; AAH03686.1; --
EMBL; BC022890; AAH22890.1; --
PIR; JC5296; JC5296.

RA Villacres E., Distèche C., Storm D.R.;
 RT "Cloning, chromosomal mapping, and regulatory properties of the human
 RT type 9 adenylyl cyclase (ADCY9).";
 RL Genomics 50:97-104(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Paterson J.M., Smith S.M., Simpson J., Grace O.C., Bell J.E.,
 RA Antoni F.A.;
 RT "Cloning and characterisation of human adenylyl cyclase IX:
 RT differential mRNA regulation and inhibition by Ca²⁺/calciuretin";
 RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Toyota T., Yamada K., Meerabux J., Hattori E., Saito K.,
 RA Yoshitsugu K., Shimizu H., Nankai M., Toru M., Detera-Wadleigh S.D.,
 RA Yoshikawa T.;
 RT "Mutation screening, case control study and transmission
 RT disequilibrium analysis of adenylyl cyclase type 9 (ADCY9) gene in
 RT functional psychoses.";
 RL Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 141-1353 FROM N.A., AND REVISION TO 1154.
 RC TISSUE=Brain;
 RX MEDLINE=22158633; PubMed=12168954;
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RT curation of 330 KIAA cDNA clones.";
 RL DNA Res. 9:99-106(2002).
 RN [5]
 RP SEQUENCE OF 788-1353 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 CC -!- FUNCTION: May play a fundamental role in situations where fine
 CC interplay between intracellular calcium and cAMP determines the
 CC cellular function. May be a physiologically relevant docking site
 CC for calcineurin (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
 CC -!- COFACTOR: Binds 2 magnesium ions per subunit.
 CC -!- ENZYME REGULATION: Insensitive to calcium/calmodulin, forskolin
 CC and somatostatin. Stimulated by beta-adrenergic receptor
 CC activation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DOMAIN: Composed of two homologous domains.
 CC -!- SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl
 CC cyclase family.
 CC -!- SIMILARITY: Contains 1 FKBP-type PPIase domain.
 CC
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 CC
 DR EMBL; AF036927; AAC24201.1; -;
 DR EMBL; AJ131123; CAB65084.1; -;
 DR EMBL; AY028959; AAK29464.1; -;
 DR EMBL; AY028949; AAK29464.1; JOINED.
 DR EMBL; AY028950; AAK29464.1; JOINED.
 DR EMBL; AY028951; AAK29464.1; JOINED.
 DR EMBL; AY028952; AAK29464.1; JOINED.
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 DR EMBL; AY028955; AAK29464.1; JOINED.
 DR EMBL; AY028956; AAK29464.1; JOINED.
 DR EMBL; AY028957; AAK29464.1; JOINED.

DR EMBL; AB011092; BAA25446.2; -;
 DR HSP; P28769; IAB8.
 DR Genew; HGNC:240; ADCY9.
 DR MIM; 603302; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004016; F:adenylyl cyclase activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR001054; G_cyclase.
 DR Pfam; PF00211; guanylate_cyc; 2.
 DR SMART; SM00044; CYCC; 2.
 DR PROSITE; PS00452; GUANYLATE_CYCLASES_2;
 DR PROSITE; PS0125; GUANYLATE_CYCLASES_1; 1.
 KW Lyase; CAMP biosynthesis; Transmembrane; Glycoprotein; Repeat;
 KW Metal-binding; Magnesium; Isomerase; Rotamase.
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 FT TRANSMEM 10322 10341 POTENTIAL.
 FT DOMAIN 10342 10361 POTENTIAL.
 FT TRAN

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|--|---|---|
| | OS | Chlamydia trachomatis. |
| | OX | Bacteria; Chlamydiaceae; Chlamydiales; Chlamydiaceae; Chlamydia. |
| | OC | NCBII_TaxID=813; |
| | RN | [1] |
| | RP | SEQUENCE FROM N.A. |
| | RC | STRAIN=D/UW-3/Cx; |
| | RA | MEDLINE=99000809; PubMed=9784136; |
| | RX | Stephens R.S., Kalman S., Lammel C.J.; Fan J., Marathe R., Aravind L., |
| | RY | Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., |
| | RA | Davis R.W.; |
| | RT | "Genome sequence of an obligate intracellular pathogen of humans: |
| | RL | Chlamydia trachomatis."; |
| | RM | Science 282:754-759(1998). |
| | RN | [2] |
| | RP | SEQUENCE OF 1-292 FROM N.A. |
| | RC | STRAIN=E/UW-5/Cx; |
| | RX | MEDLINE=94320787; PubMed=8045424; |
| | RA | Schmied D.H., Wyrick P.B.; |
| | RT | "Another putative heat-shock gene and aminoacyl-tRNA synthetase gene |
| | RL | are located upstream from the grpE-like and dnaK-like genes in |
| | RM | Chlamydia trachomatis."; |
| | RN | Gene 145:57-63(1994).; |
| | CC | -!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0499/CT392/TC0671 FAMILY. |
| | CC | ----- |
| | CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outpost - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch) |
| | CC | ----- |
| | DR | EMBL; AE001312; AAC67989.1; .. |
| | DD | EMBL; LS5105; AAA23160.1; .. |
| | DR | PfR; F71520; F71520. |
| | KW | Hypothetical protein; Complete proteome. |
| | LD | VARIANT 155 155 Y->H [IN STRAIN E/UW-5/CX]. |
| | FT | SEQUENCE 377 AA; 41449 MW; 9D7A33720000653D CRC64; |
| | SQ | Query Match 46.1%; Score 41; DB 1; Length 377; Best Local Similarity 50.0%; Pred.No.35; Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0; |
| | QY | 2 IMEKADSNKTIDE 15 : 85 VMEKDANVKLDE 98 |
| | Dd | |
| | RESULT 10 | |
| | YSH8 CAEBL | |
| | ID YSH8 CAEBL STANDARD; PRG; 437 AA. | |
| | AC Q09949; | |
| | DT 01-NOV-1997 (Rel. 35, Created) | |
| | DT 10-OCT-2003 (Rel. 42, Last sequence update) | |
| | DT 10-OCT-2003 (Rel. 42, Last annotation update) | |
| | DE Hypothetical protein FL2A10.8 in chromosome II. | |
| | GN FlA10.8. | |
| | OS Caenorhabditis elegans. | |
| | OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea; | |
| | OC Chlamydidae; Pelodierinae; Caenorbabdtitis. | |
| | OX NCBI_TaxID=6239; | |
| | RN [1] | |
| | RP SEQUENCE FROM N.A. | |
| | RC STRAIN-Bristol NZ; | |
| | RA Geisel C.; | |
| | RM Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases. | |
| | RN [2] | |
| | RP REVISIONS. | |
| | RA Waterston R.; | |
| | RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. | |
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CC or send an email to license@isb-sib.ch).

DR EMBL: U28731; AAA68301.2; --
DR PIR: T16046; T16046.
DR WormPep: F12A10.8; EC31784.
KW Hypothetical protein.
SQ SEQUENCE 437 AA; 50341 MW; BEE72C813377A6DC CRC64;

Query Match 46.1%; Score 41; DB 1; Length 437;
Best Local Similarity 61.5%; Pred. No. 40;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 KADSNKTRIDEAN 17
DB 312 KASASKPRFDEAN 324
||:|||||

RESULT 11
MCH METH STANDARD; PRT; 320 AA.
AC 026867;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE N(5).N(10)-methenyltetrahydromethanopterin cyclohydrolase
DE (EC 3.5.4.27) (Methenyl-H4MPT cyclohydrolase).
GN MCH OR MTH773.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwanji N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McQuall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -!- FUNCTION: Reversible interconversion of N(5)-formyl-H(4)MPT to
CC methenyl-H(4)MPT(+) (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methenyl-5,6,7,8-tetrahydromethanopterin
CC + H(2)O = N(5)-formyl-5,6,7,8-tetrahydromethanopterin.
CC -!- PATHWAY: Methanogenesis from carbon dioxide; third step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the MCH family.

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CC or send an email to license@isb-sib.ch).

DR EMBL: A5000856; AAB85276.1; --
DR PIR: D69203; D69203.
DR HAMAP: P94954; 1QLM.
DR HSSP: P94954; 1QLM.
DR InterPro: IPR003209; Cyclohydrolase.
DR Pfam: PF02289; MCH; 1.
DR ProDom: PD011637; Cyclohydrolase; 1.

KW Methanogenesis; One-carbon metabolism; Hydrolase; Complete proteome.
SQ SEQUENCE 320 AA; 34319 MW; C10CE736C675AA02 CRC64;

Query Match 44.9%; Score 40; DB 1; Length 320;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDE 15
DB 14 RMIEKADDLKIKVDK 28
||:|||||

RESULT 12
BNB DROME STANDARD; PRT; 442 AA.
AC P29746; Q9VWQ0;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bangles and beads protein.
DE BNG OR CG7088.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90126372; PubMed=2693037;
RA Ng S.C., Perkins L.A., Conboy G., Perrimon N., Fishman M.C.;
RT "A Drosophila gene expressed in the embryonic CNS shares one
RT conserved domain with the mammalian GAP-43.";
RL Development 105:629-638(1989).
RN [2]
RP REVISIONS.
RX MEDLINE=92201643; PubMed=1551578;
RA Eberl D.F., Perkins L.A., Engelstein M., Hilliker A.J., Perrimon N.;
RT "Genetic and developmental analysis of polytene section 17 of the X
RT chromosome of Drosophila melanogaster.";
RL Genetics 130:569-583(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mounir S.M., Moy M., Murphy B., Murphy L., Muszy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskey D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,


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CC CC -!- SUBUNIT: Generally pentameric. There are five types of GABA(A)
CC CC receptor chains: alpha, beta, gamma, delta, and rho.
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC CC -----
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CC CC -----
CC CC EMBL: X58638; CAA41495.1; --
CC CC PIR: S17785; S17785.
CC CC InterPro: IPR006029; Neu channel memb.
CC CC InterPro: IPR006202; Neur chan LBD.
CC CC InterPro: IPR006201; Neur channel.
CC CC Pfam: PF02931; Neur chan LBD; 1.
CC CC Pfam: PF02932; Neur chan memb; 1.
CC CC PRINTS: PR00252; NRIONCHANNEL.
CC CC TIGRFS: TIGR00860; LIC; 1.
CC CC PROSITE: PS00236; NEUROTR ION CHANNEL; 1.
CC CC Postsynaptic membrane; Tonic channel; Glycoprotein; Signal;
CC CC Transmembrane; Multigene family; Chloride channel.
CC CC SIGNAL 1 23 POTENTIAL.
CC CC CHAIN 24 499 GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA
CC CC FT FT SUBUNIT.
CC CC FT FT EXTRACELLULAR (PROBABLE).
CC CC FT FT PROBABLE.
CC CC FT FT PROBABLE.
CC CC FT FT PROBABLE.
CC CC FT FT CYTOPLASMIC (PROBABLE).
CC CC FT FT PROBABLE.
CC CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC FT FT BY SIMILARITY.
CC CC FT FT SEQUENCE 499 AA; 57081 MW; F81C9F2A850D62F4 CRC64;
CC CC -----
CC CC Query Match 44.9%; Score 40; DB 1; Length 499;
CC CC Best Local Similarity 38.9%; Pred.No. 67;
CC CC Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
CC CC -----
CC CC QY 1 RIMEKADSNKTRIDEANQ 18
CC CC | : | : | : | : | : |
CC CC 348 RLREAFATSVKVRDDGQ 365
CC CC -----
CC CC RESULT 14
CC CC DB2_SCHPO
CC CC ID DB2_SCHPO STANDARD; PRT; 550 AA.
CC CC AC P24782;
CC CC DT 01-MAR-1992 (Rel. 21, Created)
CC CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC CC DE P68-like protein.
CC CC GN DB2 OR SPBP87.16C.
CC CC OS Schizosaccharomyces pombe (Fission yeast).
CC CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC CC OC Schizosaccharomycetes.
CC CC OX NCBI_TaxID=4896;
CC CC [1] --
CC CC RP SEQUENCE FROM N.A.
CC CC RX MEDLINE-91141480; PubMed=1996094;
CC CC RA Iggo R.D., Jamieson D.J., McNeill S.A., Southgate J., McPheat J.,
CC CC Lane D.P.;
CC CC RA "p68 RNA helicase: identification of a nucleolar form and cloning of
CC CC RT related genes containing a conserved intron in yeasts.";
CC CC RL Mol. Cell. Biol. 11:1326-1333(1991).
CC CC RN [2]

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Query Match 44.9%; Score 40; DB 1; Length 550;
Best Local Similarity 34.6%; Pred. No. 74;
Matches 9; Conservative 6; Mismatches 3; Indels 8; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:36 ; Search time 13.1351 Seconds
(without alignments)
131.818 Million cell updates/sec

Title: US-10-030-485A-5

Perfect score: 89
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 89 | 100.0 | 204 | 2 I50480 | synapse protein SN |
| 2 | 89 | 100.0 | 206 | 2 A37861 | synaptosomal-assoc |
| 3 | 89 | 100.0 | 206 | 2 I53735 | nerve terminal pro |
| 4 | 89 | 100.0 | 206 | 2 I67823 | nerve terminal pro |
| 5 | 89 | 100.0 | 206 | 2 A33623 | synaptosomal-assoc |
| 6 | 80 | 89.9 | 203 | 2 I50481 | synapse protein SN |
| 7 | 50 | 67.4 | 210 | 2 I50552 | synapse protein - |
| 8 | 59 | 66.3 | 210 | 2 JC5512 | SNARE protein 23 - |
| 9 | 55 | 61.8 | 158 | 2 JC5297 | vesicle-membrane f |
| 10 | 55 | 61.8 | 211 | 2 JC5296 | vesicle-membrane f |
| 11 | 54 | 60.7 | 29 | 2 A49708 | synaptosomal-assoc |
| 12 | 50 | 56.2 | 234 | 2 T26553 | hypothetical prote |
| 13 | 45 | 50.6 | 1138 | 2 T24635 | hypothetical prote |
| 14 | 43 | 48.3 | 401 | 2 E81436 | transmembrane tran |
| 15 | 43 | 48.3 | 480 | 2 T18905 | hypothetical prote |
| 16 | 42 | 47.2 | 173 | 2 T38231 | hypothetical prote |
| 17 | 41 | 46.1 | 141 | 2 T33983 | hypothetical prote |
| 18 | 41 | 46.1 | 285 | 2 A03576 | fusaric acid resis |
| 19 | 41 | 46.1 | 238 | 1 S40743 | 3-hydroxyacyl-CoA |
| 20 | 41 | 46.1 | 318 | 2 B90399 | probable acyl-coen |
| 21 | 41 | 46.1 | 377 | 2 T71520 | hypothetical prote |
| 22 | 41 | 46.1 | 393 | 2 T16046 | hypothetical prote |
| 23 | 41 | 46.1 | 554 | 2 F86244 | hypothetical prote |
| 24 | 41 | 46.1 | 575 | 2 F96966 | hypothetical prote |
| 25 | 41 | 46.1 | 642 | 2 G90551 | lipoprotein [impor |
| 26 | 41 | 46.1 | 2541 | 2 T29340 | hypothetical prote |
| 27 | 40.5 | 45.5 | 228 | 2 B89776 | capsular polysacch |
| 28 | 40 | 44.9 | 300 | 2 H75200 | hypothetical prote |
| 29 | 40 | 44.9 | 300 | 2 D71234 | hypothetical prote |

30 40 44.9 320 2 D69203 methenyltetrahydro
31 40 44.9 362 2 T49090 hypothetical prote
32 40 44.9 409 2 D90182 lps biosynthesis p
33 40 44.9 441 2 A43555 GAP-43-related pro
34 40 44.9 499 2 S17785 gamma-aminobutyric
35 40 44.9 550 1 S14048 RNA helicase dbp2
36 40 44.9 689 2 T25202 hypothetical prote
37 40 44.9 1031 2 A12589 DNA polymerase I
38 40 44.9 1031 2 B97372 DNA polymerase I
39 40 44.9 1252 2 B42771 reticulocyte-bind
40 40 44.9 1254 2 E86160 hypothetical prote
41 40 44.9 1787 2 AG3360 probable tape-meas
42 39.5 44.4 668 1 UYPVCP noncapsid protein
43 39.5 44.4 668 1 UYPVCP noncapsid protein
44 39 43.8 117 2 G82982 conserved hypothet
45 39 43.8 225 2 T28319 ORF MSV158 probabl

ALIGNMENTS

RESULT 1
I50480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50480
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-204 <RIS>
A:Cross-references: GB:L22973; NID:g349426; PIDN:AAA16537.1; PID:g349427
C:Genetics:
A:Gene: SNAP-25

Query Match 100.0%; Score 89; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
DB 178 RIMEKADSNKTRIDEANQ 195
|||||

RESULT 2

A37861
synaptosomal-associated 25K protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:Catascas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coinci
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
DB 180 RIMEKADSNKTRIDEANQ 197
|||||

RESULT 3

153735
Query Match 100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C:Species: Homo sapiens (human)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:L19760; NID:G307425; PIDN:AAC37545.1; PID:G307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
DB 180 RIMEKADSNKTRIDEANQ 197

RESULT 4

I67823
Query Match 100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C:Species: Homo sapiens (human)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:L19761; NID:G307427; PIDN:AAC37546.1; PID:G307428
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
DB 180 RIMEKADSNKTRIDEANQ 197

RESULT 5

A33623
Query Match 100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C:Species: Mus musculus (house mouse)
C>Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differ
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M22012; GB:X51673; NID:G200997; PIDN:AAA61741.1; PID:G200998

Query Match

100.0%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
DB 180 RIMEKADSNKTRIDEANQ 197

RESULT 6

I50481
Query Match 100.0%; Score 89; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
C:Species: Carassius auratus (goldfish)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50481
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50481
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RIS>
A:Cross-references: GB:L22976; NID:G349430; PIDN:AAA16538.1; PID:G349431
C:Genetics:
A:Gene: SNAP-25

Query Match

89.9%; Score 80; DB 2; Length 203;
Best Local Similarity 88.9%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
DB 177 RIMEKADSNKTRIDEANQ 194

RESULT 7

I50552
Query Match 89.9%; Score 80; DB 2; Length 203;
Best Local Similarity 88.9%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
C:Species: Torpedo marmorata (marbled electric ray)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50552
R:Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nasseel, D.; Pieribone, V.
J. Biol. Chem. 268, 24408-24414, 1993
A:Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) s
A:Reference number: A49513; MUID:94043281; PMID:8226991
A:Accession: I50552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-210 <RIS>
A:Cross-references: GB:L22020; NID:G431296; PIDN:AAA49284.1; PID:G431297

Query Match

67.4%; Score 60; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 0.026;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
DB 187 RIVVKGDMKARIDEANK 204

RESULT 8

JC5512
Query Match 67.4%; Score 60; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 0.026;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
C:Species: Mus musculus (house mouse)
C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5512
R:Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Ok
Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A:Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A:Reference number: JC5512; MUID:97312558; PMID:9168999
A:Accession: JC5512

A:Molecule type: mRNA
A:Residues: 1-210 <RA>
A:Cross-references: DDBJ:AB000822; NID:g2189950; PIDN:BAA20345.1; PID:d1021177; PID:g2189950
C:Comment: This protein is involved in the insulin-induced translocation of vesicles containing syntaxin 1A

Query Match 66.3%; Score 59; DB 2; Length 210;
Best Local Similarity 70.6%; Pred. No. 0.038;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
DB 185 KITEKADTNKRIDIAN 201
|||:|||||
|||:|||||

RESULT 9
JC5297
vesicle-membrane fusion protein SNAP-23B - human
C:Species: Homo sapiens (man)
C:Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C:Accession: JC5297
R:Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A:Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23B
A:Reference number: JC5296; MUID:97224437; PMID:9070898
A:Accession: JC5297
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-158 <MOL>
A:Cross-references: GB:Y09569; NID:g1924943; PIDN:CAA70761.1; PID:e290774; PID:g1924944
A:Experimental source: neutrophils
C:Comment: This protein is involved in regulating exocytosis in human neutrophils, a cell type that contains a large number of secretory granules

Query Match 61.8%; Score 55; DB 2; Length 158;
Best Local Similarity 64.7%; Pred. No. 0.13;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
DB 133 RITDKADTNKRIDIAN 149
|||:|||||
|||:|||||

RESULT 10
JC5296
vesicle-membrane fusion protein SNAP-23A - human
C:Species: Homo sapiens (man)
C:Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C:Accession: JC5296
R:Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A:Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23A
A:Reference number: JC5296; MUID:97224437; PMID:9070898
A:Accession: JC5296
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-211 <MOL>
A:Cross-references: GB:Y09567; NID:g1924941; PIDN:CAA70760.1; PID:e290695; PID:g1924942
C:Comment: This protein is involved in regulating exocytosis in human neutrophils, a cell type that contains a large number of secretory granules

Query Match 61.8%; Score 55; DB 2; Length 211;
Best Local Similarity 64.7%; Pred. No. 0.17;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
DB 186 RITDKADTNKRIDIAN 202
|||:|||||
|||:|||||

RESULT 11
A49708
synaptosomal-associated 25K protein - rat (fragments)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
C:Accession: A49708

R:Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; J. Biol. Chem. 269, 1617-1620, 1994
A:Title: Proteolysis of SNAP-25 by types E and A botulinum neurotoxins.
A:Reference number: A49708; MUID:94124495; PMID:8294407
A:Accession: A49708
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <BIN>

Query Match 60.7%; Score 54; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IMEKADSNKTR 12
DB 11 IMEKADSNKTR 21
|||||
|||||

RESULT 12
T26553
hypothetical protein Y22F5A.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26553
R:Gardner, A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20231
A:Accession: T26553
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-234 <WIL>
A:Cross-references: EMBL:AL021479; PIDN:CAAL6322.1; GSPDB:GN00023; CESP:Y22F5A.3
A:Experimental source: clone Y22F5A
C:Genetics:
A:Gene: CESP:Y22F5A.3
A:Map position: 5
A:Introns: 51/3; 82/1; 165/2; 213/3

Query Match 56.2%; Score 50; DB 2; Length 234;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
DB 209 RIHDKAQSNVRVESANK 226
|||:|||||
|||:|||||

RESULT 13
T24635
hypothetical protein T07C4.10a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C:Accession: T24635; S41023
R:Buck, D.
submitted to the EMBL Data Library, February 1995
A:Reference number: Z19915
A:Accession: T24635
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1138 <WIL>
A:Cross-references: EMBL:Z48055; PIDN:CAA88136.1; GSPDB:GN00021; CESP:T07C4.10a
A:Experimental source: clone T07A5
R:Birks, M.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41014
A:Accession: S41023
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 895-1138 <BER>
A:Cross-references: EMBL:Z29443
C:Genetics:
A:Gene: CESP:T07C4.10a
A:Map position: 3

Job time : 14.1351 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:07:42 ; Search time 26.7568 Seconds
(without alignments)
142.049 Million cell updates/sec

Title: US-10-030-485A-5
Perfect score: 89
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 89 | 100.0 | 33 | 10 | US-09-942-024-33 |
| 2 | 89 | 100.0 | 33 | 10 | US-09-942-024-38 |
| 3 | 89 | 100.0 | 33 | 10 | US-09-942-098-33 |
| 4 | 89 | 100.0 | 33 | 10 | US-09-942-098-38 |
| 5 | 89 | 100.0 | 116 | 10 | US-09-962-360B-11 |
| 6 | 89 | 100.0 | 116 | 10 | US-09-962-360B-12 |
| 7 | 89 | 100.0 | 206 | 10 | US-09-942-024-2 |
| 8 | 89 | 100.0 | 206 | 10 | US-09-942-024-7 |
| 9 | 89 | 100.0 | 206 | 10 | US-09-942-024-12 |
| 10 | 89 | 100.0 | 206 | 10 | US-09-942-098-2 |
| 11 | 89 | 100.0 | 206 | 10 | US-09-942-098-7 |
| 12 | 89 | 100.0 | 206 | 10 | US-09-942-098-12 |
| 13 | 80 | 89.9 | 33 | 10 | US-09-942-024-37 |
| 14 | 80 | 89.9 | 33 | 10 | US-09-942-098-37 |
| 15 | 80 | 89.9 | 203 | 10 | US-09-942-024-14 |

| | | | | | | |
|----|----|------|-----|----|------------------|-------------------|
| 16 | 80 | 89.9 | 203 | 10 | US-09-942-098-14 | Sequence 14, Appl |
| 17 | 65 | 73.0 | 21 | 10 | US-09-942-024-89 | Sequence 89, Appl |
| 18 | 65 | 73.0 | 21 | 10 | US-09-942-098-89 | Sequence 89, Appl |
| 19 | 65 | 73.0 | 24 | 10 | US-09-942-024-90 | Sequence 90, Appl |
| 20 | 65 | 73.0 | 24 | 10 | US-09-942-098-90 | Sequence 90, Appl |
| 21 | 61 | 68.5 | 13 | 10 | US-09-942-024-86 | Sequence 86, Appl |
| 22 | 61 | 68.5 | 13 | 10 | US-09-942-098-86 | Sequence 86, Appl |
| 23 | 61 | 68.5 | 17 | 10 | US-09-942-024-31 | Sequence 31, Appl |
| 24 | 61 | 68.5 | 17 | 10 | US-09-942-098-31 | Sequence 31, Appl |
| 25 | 61 | 68.5 | 18 | 10 | US-09-942-024-32 | Sequence 32, Appl |
| 26 | 61 | 68.5 | 18 | 10 | US-09-942-098-32 | Sequence 32, Appl |
| 27 | 61 | 68.5 | 23 | 10 | US-09-942-024-88 | Sequence 88, Appl |
| 28 | 61 | 68.5 | 23 | 10 | US-09-942-098-88 | Sequence 88, Appl |
| 29 | 60 | 67.4 | 30 | 10 | US-09-942-024-39 | Sequence 39, Appl |
| 30 | 60 | 67.4 | 30 | 10 | US-09-942-098-39 | Sequence 39, Appl |
| 31 | 59 | 66.3 | 32 | 10 | US-09-942-024-35 | Sequence 35, Appl |
| 32 | 59 | 66.3 | 32 | 10 | US-09-942-098-35 | Sequence 35, Appl |
| 33 | 55 | 61.8 | 15 | 10 | US-09-942-024-28 | Sequence 28, Appl |
| 34 | 55 | 61.8 | 15 | 10 | US-09-942-098-28 | Sequence 28, Appl |
| 35 | 55 | 61.8 | 16 | 10 | US-09-942-024-29 | Sequence 29, Appl |
| 36 | 55 | 61.8 | 16 | 10 | US-09-942-098-29 | Sequence 29, Appl |
| 37 | 55 | 61.8 | 17 | 10 | US-09-942-024-30 | Sequence 30, Appl |
| 38 | 55 | 61.8 | 17 | 10 | US-09-942-098-30 | Sequence 30, Appl |
| 39 | 55 | 61.8 | 17 | 10 | US-09-942-024-45 | Sequence 45, Appl |
| 40 | 55 | 61.8 | 17 | 10 | US-09-942-098-45 | Sequence 45, Appl |
| 41 | 55 | 61.8 | 17 | 10 | US-09-942-024-47 | Sequence 47, Appl |
| 42 | 55 | 61.8 | 17 | 10 | US-09-942-098-47 | Sequence 47, Appl |
| 43 | 55 | 61.8 | 17 | 10 | US-09-942-024-49 | Sequence 49, Appl |
| 44 | 55 | 61.8 | 17 | 10 | US-09-942-098-49 | Sequence 49, Appl |
| 45 | 55 | 61.8 | 17 | 10 | US-09-942-024-44 | Sequence 44, Appl |

ALIGNMENTS

RESULT 1
US-09-942-024-33
; Sequence 33, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942.024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-33

Query Match 100.0%; Score 89; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
|||||
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 2
US-09-942-024-38
; Sequence 38, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-38

Query Match 100.0%; Score 89; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 3

US-09-942-098-33
; Sequence 33, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33

Query Match 100.0%; Score 89; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 4

US-09-942-098-38
; Sequence 38, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-38

Query Match 100.0%; Score 89; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
Db 7 RIMEKADSNKTRIDEANQ 24

RESULT 5

US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11

Query Match 100.0%; Score 89; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
Db 89 RIMEKADSNKTRIDEANQ 106

RESULT 6

US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1

; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-942-024-12

Query Match 100.0%; Score 89; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 89 RIMEKADSNKTRIDEANQ 106
|||||

RESULT 7

US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-942-024-2

Query Match 100.0%; Score 89; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 180 RIMEKADSNKTRIDEANQ 197
|||||

RESULT 8

US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.

US-09-942-024-7

Query Match 100.0%; Score 89; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 180 RIMEKADSNKTRIDEANQ 197
|||||

RESULT 9

US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-942-024-12

Query Match 100.0%; Score 89; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 180 RIMEKADSNKTRIDEANQ 197
|||||

RESULT 10

US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-942-098-2

Query Match 100.0%; Score 89; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 180 RIMEKADSNKTRIDEANQ 197
|||||

RESULT 11

US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

Query Match 100.0%; Score 89; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
|||: |||||
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 12

; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match 100.0%; Score 89; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
|||: |||||
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 13

; Sequence 37, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-37

Query Match 89.9%; Score 80; DB 10; Length 33;
Best Local Similarity 88.9%; Pred. No. 3.6e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
|||: |||||

Db 7 RIMWADSNKTRIDEANQ 24

RESULT 14

US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.

; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-37

Query Match 89.9%; Score 80; DB 10; Length 33;
Best Local Similarity 88.9%; Pred. No. 3.6e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
|||: |||||
Db 7 RIMWADSNKTRIDEANQ 24

RESULT 15

US-09-942-024-14
; Sequence 14, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.

; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-14

Query Match 89.9%; Score 80; DB 10; Length 203;
Best Local Similarity 88.9%; Pred. No. 2.9e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RIMEKADSNKTRIDEANQ 18
|||: |||||
Db 177 RIMWADSNKTRIDEANQ 194

Search completed: March 9, 2004, 11:12:07
Job time : 27.7568 secs

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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:05:46 ; Search time 16.0541 Seconds
(without alignments)
57.884 Million cell updates/sec

Title: US-10-030-485A-5
Perfect score: 89
Sequence: 1 RIMEXADSNKTRIDEANQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 89 | 100.0 | 37 | 3 | US-08-819-286-4 |
| 2 | 89 | 100.0 | 70 | 2 | US-08-760-001-10 |
| 3 | 89 | 100.0 | 70 | 3 | US-09-015-960-10 |
| 4 | 89 | 100.0 | 70 | 4 | US-09-534-572-10 |
| 5 | 89 | 100.0 | 206 | 1 | US-08-393-985-18 |
| 6 | 89 | 100.0 | 206 | 3 | US-08-819-286-1 |
| 7 | 84 | 94.4 | 26 | 3 | US-08-819-286-8 |
| 8 | 55 | 61.8 | 15 | 2 | US-08-743-894B-38 |
| 9 | 55 | 61.8 | 16 | 2 | US-08-743-894B-49 |
| 10 | 55 | 61.8 | 17 | 2 | US-08-743-894B-1 |
| 11 | 55 | 61.8 | 17 | 2 | US-08-743-894B-24 |
| 12 | 55 | 61.8 | 17 | 2 | US-08-743-894B-25 |
| 13 | 55 | 61.8 | 17 | 2 | US-08-743-894B-26 |
| 14 | 55 | 61.8 | 17 | 2 | US-08-743-894B-27 |
| 15 | 55 | 61.8 | 17 | 2 | US-08-743-894B-28 |
| 16 | 55 | 61.8 | 17 | 2 | US-08-743-894B-31 |
| 17 | 55 | 61.8 | 17 | 2 | US-08-743-894B-32 |
| 18 | 55 | 61.8 | 17 | 2 | US-08-743-894B-37 |
| 19 | 55 | 61.8 | 17 | 2 | US-08-743-894B-39 |
| 20 | 55 | 61.8 | 17 | 2 | US-08-743-894B-42 |
| 21 | 55 | 61.8 | 17 | 2 | US-08-743-894B-43 |
| 22 | 55 | 61.8 | 17 | 2 | US-08-743-894B-44 |
| 23 | 55 | 61.8 | 17 | 2 | US-08-743-894B-45 |
| 24 | 55 | 61.8 | 17 | 2 | US-08-743-894B-47 |
| 25 | 55 | 61.8 | 20 | 3 | US-08-819-286-9 |
| 26 | 52 | 58.4 | 16 | 2 | US-08-743-894B-51 |
| 27 | 52 | 58.4 | 16 | 2 | US-08-743-894B-52 |

| | | | | | |
|----|----|------|----|---|-------------------|
| 28 | 52 | 58.4 | 16 | 2 | US-08-743-894B-54 |
| 29 | 52 | 58.4 | 17 | 2 | US-08-743-894B-2 |
| 30 | 52 | 58.4 | 17 | 2 | US-08-743-894B-5 |
| 31 | 52 | 58.4 | 17 | 2 | US-08-743-894B-6 |
| 32 | 52 | 58.4 | 17 | 2 | US-08-743-894B-18 |
| 33 | 51 | 57.3 | 17 | 2 | US-08-743-894B-30 |
| 34 | 50 | 56.2 | 17 | 2 | US-08-743-894B-19 |
| 35 | 50 | 56.2 | 17 | 2 | US-08-743-894B-29 |
| 36 | 50 | 56.2 | 17 | 2 | US-08-743-894B-33 |
| 37 | 50 | 56.2 | 17 | 2 | US-08-743-894B-34 |
| 38 | 50 | 56.2 | 17 | 2 | US-08-743-894B-48 |
| 39 | 50 | 56.2 | 17 | 2 | US-08-743-894B-50 |
| 40 | 49 | 55.1 | 16 | 2 | US-08-743-894B-12 |
| 41 | 49 | 55.1 | 16 | 3 | US-08-819-286-12 |
| 42 | 49 | 55.1 | 17 | 2 | US-08-743-894B-3 |
| 43 | 49 | 55.1 | 17 | 2 | US-08-743-894B-20 |
| 44 | 49 | 55.1 | 17 | 2 | US-08-743-894B-36 |
| 45 | 49 | 55.1 | 17 | 2 | US-08-743-894B-46 |

ALIGNMENTS

RESULT 1
US-08-819-286-4
; Sequence 4, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-4

Query Match 100.0%; Score 89; DB 3; Length 37;
Best Local Similarity 100.0%; Pred.No 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIMEXADSNKTRIDEANQ 18
|||||

Db 11 RIMEXADSNKTRIDEANQ 28

RESULT 2

US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637

GENERAL INFORMATION:

; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

; ZIP: 20005-3934

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760.001
; FILING DATE: Herewith
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:

; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-760-001-10

Query Match 100.0%; Score 89; DB 2; Length 70;

Best Local Similarity 100.0%; Pred. No. 3e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEXADSNKTRIDEANQ 18

Db 44 RIMEXADSNKTRIDEANQ 61

RESULT 3

US-09-015-960-10

; Sequence 10, Application US/09015960
; Patent No. 6043042

GENERAL INFORMATION:

; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington

; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015.960
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760.001
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-015-960-10

Query Match 100.0%; Score 89; DB 1; Length 70;

Best Local Similarity 100.0%; Pred. No. 3e-08; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEXADSNKTRIDEANQ 18

Db 44 RIMEXADSNKTRIDEANQ 61

RESULT 4

US-09-534-572-10

; Sequence 10, Application US/09534572
; Patent No. 6337386

GENERAL INFORMATION:

; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

; ZIP: 20005-3934

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534.572
; FILING DATE: Herewith

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015.960
; FILING DATE: 30-JAN-1998

ATTORNEY/AGENT INFORMATION:

; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-534-572-10

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-534-572-10

Query Match      100.0%; Score 89; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIMEKADSNKTRIDEANQ 18
DB      44 RIMEKADSNKTRIDEANQ 61

RESULT 5
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Schellier, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match      100.0%; Score 89; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIMEKADSNKTRIDEANQ 18
DB      1 RIMEKADSNKTRIDEANQ 18
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-534-572-10

Query Match      100.0%; Score 89; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIMEKADSNKTRIDEANQ 18
DB      44 RIMEKADSNKTRIDEANQ 61

RESULT 5
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Schellier, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match      100.0%; Score 89; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIMEKADSNKTRIDEANQ 18
DB      1 RIMEKADSNKTRIDEANQ 18
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-8

Query Match 94.4%; Score 84; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IMEKADSNKTRIDEANQ 18
DB 1 IMEKADSNKTRIDEANQ 17

RESULT 8
US-08-743-894B-38
; Sequence 38, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-49

Query Match 61.8%; Score 55; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SNKTRIDEANQ 18
DB 1 SNKTRIDEANQ 11

RESULT 9
US-08-743-894B-49
; Sequence 49, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-49

Query Match 61.8%; Score 55; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SNKTRIDEANQ 18
DB 1 SNKTRIDEANQ 11

RESULT 10
US-08-743-894B-1
; Sequence 1, Application US/08743894B
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-38

Query Match 61.8%; Score 55; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SNKTRIDEANQ 18
DB 1 SNKTRIDEANQ 11

RESULT 9
US-08-743-894B-49
; Sequence 49, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-49

Query Match 61.8%; Score 55; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SNKTRIDEANQ 18
DB 1 SNKTRIDEANQ 11

RESULT 10
US-08-743-894B-1
; Sequence 1, Application US/08743894B
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; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-743-894B-1
;
; Query Match 61.8%; Score 55; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.0037;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 SNKTRIDEANQ 18
; DB 1 SNKTRIDEANQ 11
;
; RESULT 11
; US-08-743-894B-24
; Sequence 24, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-24
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 16
; OTHER INFORMATION: Xaa represents norleucine
; US-08-743-894B-24
;
; Query Match 61.8%; Score 55; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.0037;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 8 SNKTRIDEANQ 18
; DB 1 SNKTRIDEANQ 11
;
; RESULT 12
; US-08-743-894B-25
; Sequence 25, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin f
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-25
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
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US-08-743-894B-28

Query Match 61.8%; Score 55; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 8 SNKTRIDEANQ 18
Db 1 SNKTRIDEANQ 11

Search completed: March 9, 2004, 11:10:59
Job time : 16.0541 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2004, 10:57:21 ; Search time 49.6216 Seconds
(without alignments)
102.493 Million cell updates/sec

Title: US-10-030-485A-5

Perfect score: 89
Sequence: 1 RIMEKADSNKTRIDENQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|----------|--------------------|
| 1 | 89 | 100.0 | 18 | 4 | AAB15585 | Aab15585 Human SNA |
| 2 | 89 | 100.0 | 33 | 6 | AAE36683 | AAE36683 GOLdfish |
| 3 | 89 | 100.0 | 33 | 6 | AAE36678 | AAE36678 SNAP-25 p |
| 4 | 89 | 100.0 | 37 | 2 | AAW30097 | AAW30097 Neurotran |
| 5 | 89 | 100.0 | 70 | 2 | AAE86823 | AAE86823 SNAP-25 r |
| 6 | 89 | 100.0 | 86 | 4 | AAE15584 | AAE15584 Human SNA |
| 7 | 89 | 100.0 | 116 | 5 | AAO15165 | AAO15165 Clostridi |
| 8 | 89 | 100.0 | 116 | 5 | AAO15166 | AAO15166 Clostridi |
| 9 | 89 | 100.0 | 198 | 4 | AAU00255 | AAU00255 Synaptoso |
| 10 | 89 | 100.0 | 199 | 4 | AAU00263 | AAU00263 Synaptoso |
| 11 | 89 | 100.0 | 200 | 4 | AAU00264 | AAU00264 Synaptoso |
| 12 | 89 | 100.0 | 201 | 4 | AAU02637 | AAU02637 Synaptoso |
| 13 | 89 | 100.0 | 202 | 4 | AAU00265 | AAU00265 Synaptoso |
| 14 | 89 | 100.0 | 203 | 4 | AAU02636 | AAU02636 Synaptoso |
| 15 | 89 | 100.0 | 206 | 2 | AAW30103 | AAW30103 Synaptoso |
| 16 | 89 | 100.0 | 206 | 2 | AAW43426 | AAW43426 Mouse syn |
| 17 | 89 | 100.0 | 206 | 2 | AAW79198 | AAW79198 Mouse SNA |
| 18 | 89 | 100.0 | 206 | 4 | AAU00261 | AAU00261 Synaptoso |
| 19 | 89 | 100.0 | 206 | 4 | AAU00246 | AAU00246 Synaptoso |
| 20 | 89 | 100.0 | 206 | 4 | AAU00253 | AAU00253 SNARE hom |
| 21 | 89 | 100.0 | 206 | 4 | AAU02171 | AAU02171 Synaptoso |
| 22 | 89 | 100.0 | 206 | 4 | AAU02640 | AAU02640 Synaptoso |
| 23 | 89 | 100.0 | 206 | 4 | AAU00259 | AAU00259 Synaptoso |
| 24 | 89 | 100.0 | 206 | 4 | AAU00252 | AAU00252 SNARE hom |
| 25 | 89 | 100.0 | 206 | 4 | AAU02638 | AAU02638 Synaptoso |

| | | | | | | |
|----|----|-------|-----|---|----------|--------------------|
| 26 | 89 | 100.0 | 206 | 4 | AAU02639 | AAU02639 Synaptoso |
| 27 | 89 | 100.0 | 206 | 6 | AAE36662 | AAE36662 Human SNA |
| 28 | 89 | 100.0 | 206 | 6 | AAE36667 | AAE36667 Rat VAMP- |
| 29 | 89 | 100.0 | 206 | 7 | AAE54280 | AAE54280 Rat Prote |
| 30 | 89 | 100.0 | 206 | 7 | AAE54288 | AAE54288 Rat Prote |
| 31 | 89 | 100.0 | 206 | 7 | AAE54276 | AAE54276 Rat Prote |
| 32 | 89 | 100.0 | 206 | 7 | AAE54290 | AAE54290 Human Pro |
| 33 | 89 | 100.0 | 206 | 7 | AAE54282 | AAE54282 Rat Prote |
| 34 | 89 | 100.0 | 206 | 7 | AAE54274 | AAE54274 Rat Prote |
| 35 | 89 | 100.0 | 206 | 7 | AAE54286 | AAE54286 Human Pro |
| 36 | 89 | 100.0 | 206 | 7 | AAE54284 | AAE54284 Rat Prote |
| 37 | 89 | 100.0 | 206 | 7 | AAE54272 | AAE54272 Rat Prote |
| 38 | 89 | 100.0 | 206 | 7 | AAE54278 | AAE54278 Rat Prote |
| 39 | 85 | 95.5 | 206 | 4 | AAU00266 | AAU00266 Synaptoso |
| 40 | 85 | 95.5 | 206 | 4 | AAU00262 | AAU00262 Synaptoso |
| 41 | 84 | 94.4 | 26 | 2 | AAW30099 | AAW30099 Neurotran |
| 42 | 84 | 94.4 | 206 | 4 | AAU00256 | AAU00256 Synaptoso |
| 43 | 84 | 94.4 | 206 | 4 | AAU00258 | AAU00258 Synaptoso |
| 44 | 84 | 94.4 | 206 | 4 | AAU00260 | AAU00260 Synaptoso |
| 45 | 84 | 94.4 | 206 | 4 | AAU00257 | AAU00257 Synaptoso |

ALIGNMENTS

RESULT 1
AAB15585
ID AAB15585 standard; peptide; 18 AA.
XX
AC AAB15585;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #5.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
PA (LIPO-) LIPOTEC SA.
XX
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX
DR WPI; 2001-007091/01.
XX
PT New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.
XX
PS Claim 17; Page 33; 40pp; Spanish.
XX
CC The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC disorders and pathological neuronal exocytosis-mediated pathological
CC neurodegenerative disorders
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 89; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 |||||
 DB 1 RIMEKADSNKTRIDEANQ 18

RESULT 2
 AAE36683
 ID AAE36683 standard; peptide; 33 AA.
 XX
 AC AAE36683;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Goldfish SNAP-25B peptide.
 XX
 KW Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW TeNT; cosmetic.
 XX
 OS Carassius auratus.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"
 XX
 PN WO2003020948-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 22-AUG-2002; 2002WO-US027145.
 XX
 PR 28-AUG-2001; 2001US-00942024.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX
 DR WPI; 2003-290198/28.
 XX
 PS Disclosure; Page 42; 168pp; English.
 XX
 CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridium toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridium toxin or having one or more symptoms of a
 CC clostridium toxin, to follow activity during production and purification
 CC of clostridium toxin and to assay formulated clostridium toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish

CC SNAP-25B peptide used in the invention
 XX
 SQ Sequence 33 AA;
 Query Match 100.0%; Score 89; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 |||||
 DB 7 RIMEKADSNKTRIDEANQ 24

RESULT 3
 AAE36678
 ID AAE36678 standard; peptide; 33 AA.
 XX
 AC AAE36678;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE SNAP-25 peptide.
 XX
 KW Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic; mouse; rat.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"
 XX
 PN WO2003020948-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 22-AUG-2002; 2002WO-US027145.
 XX
 PR 28-AUG-2001; 2001US-00942024.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX
 DR WPI; 2003-290198/28.
 XX
 PS Disclosure; Page 42; 168pp; English.
 XX
 CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridium toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridium toxin or having one or more symptoms of a
 CC clostridium toxin, to follow activity during production and purification
 CC of clostridium toxin and to assay formulated clostridium toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish

CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25
 CC peptide used in the invention

XX SQ Sequence 33 AA;

Query Match 100.0%; Score 89; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 |||||
 DB 7 RIMEKADSNKTRIDEANQ 24

RESULT 4

AAW30097 ID AAW30097 standard; peptide; 37 AA.

XX AC AAW30097;

XX DT 06-APR-1998 (first entry)

XX DE Neurotransmitter secretion inhibitor #1.

XX KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 XX KW excitation-secretory uncoupling peptide; catecholamine secretion;
 XX KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 XX KW synaptosomal associated protein; SNAP-25.

XX OS Homo sapiens.

XX PN WO9734620-A1.

XX PD 25-SEP-1997.

XX PF 18-MAR-1997; 97WO-US004393.

XX PR 18-MAR-1996; 96US-0013599P.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Montal M;

XX PS WPI; 1997-479986/44.

XX PT Excitation-secretory uncoupling peptide(s) for inhibiting

PT neurotransmitter release - used particularly for treating muscle

PT spasticity, and for delivering drugs specifically to neural cells.

XX PS Claim 1; Page 30; 61pp; English.

XX CC This sequence corresponds to residues 170-206 of the human 25 kD
 CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of
 CC the invention. The agents of the invention inhibit secretion of
 CC neurotransmitter from neuronal cells and is an excitation-secretory
 CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
 CC correspond substantially to any one of AAW30097-W30102, or more generally
 CC any (I) that inhibits 50% of catecholamine secretion from bovine
 CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
 CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
 CC release of neurotransmitters from synaptic vesicles, specifically for
 CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
 CC imaging of intracellular distribution of (I). Compounds for delivering
 CC the drug to neural cells provide targeted drug delivery, e.g. of
 CC substance P to brain tumours for induction of apoptosis. Unlike the
 CC neurotoxins, (I) are not toxic or immunogenic and are more readily
 CC available. Their therapeutic effect lasts for several days or weeks, so
 CC lower doses or less frequent treatments are required

SQ Sequence 37 AA;

Query Match 100.0%; Score 89; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 |||||
 DB 11 RIMEKADSNKTRIDEANQ 28

RESULT 5

AAW86823 ID AAW86823 standard; peptide; 70 AA.

XX AC AAW86823;

XX DT 15-AUG-1996 (first entry)

XX DE SNAP-25 residues 137-206.

XX KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
 XX KW neurotransmitter; neurotoxin; botulinum; cleavage; substrate;
 XX KW antibody; detection; assay.

XX OS Synthetic.

XX PN WO9533850-A1.

XX PD 14-DEC-1995.

XX PF 02-JUN-1995; 95WO-GB001279.

XX PR 03-JUN-1994; 94GB-00011138.

XX PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
 XX PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.

XX PI Shone CC, Hallis B, James BAF, Quinn CP;

XX DR WPI; 1996-040249/04.

XX PT Assay for botulinum or tetanus toxin - by combining test cpd. with
 PT substrate which is cleaved by the toxin, and antibody specific for the
 PT cleaved but not uncleaved substrate.

XX PS Example 4; Page 19; 48pp; English.

XX CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
 CC activities within their light sub-units. Depending on the neurotoxin type
 CC these act to cleave small proteins within the nerve cell which are
 CC involved in neurotransmitter release. Antibodies are used in assays which
 CC detect cleaved but not uncleaved substrate. Assays for botulinum types A
 CC and E use the present sequence as a substrate. The sequence is SNAP-25
 CC protein, residues 137-206

SQ Sequence 70 AA;

Query Match 100.0%; Score 89; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 |||||
 DB 44 RIMEKADSNKTRIDEANQ 61

RESULT 6

AAW15584 ID AAW15584 standard; peptide; 86 AA.

XX AC AAW15584;

DT 02-MAR-2001 (first entry)
 XX Human SNAP-25 N-terminal peptide #4.
 DE Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
 XX SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
 KW neurodegenerative disorder.
 KW Homo sapiens.
 OS WO200064932-A1.
 XX 02-NOV-2000.
 XX 18-FEB-2000; 2000MO-ES000058.
 XX 23-APR-1999; 99ES-00000844.
 XX (LIPO-) LIPOTEC SA.
 XX Blanes Mira MC, Liobregat Hernandez MM, Gil Tebar AI;
 PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
 PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
 PI Perez Paya E;
 XX WPI; 2001-007091/01.
 XX New peptides containing amino acid sequences from known proteins for
 FT treatment of neurological disorders.
 XX Claim 16; Page 32-33; 40pp; Spanish.
 XX The invention relates to new peptides comprising 3-30 contiguous amino
 CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
 CC protein 25). The peptides AAB15581-B15586 represent examples of the
 CC peptides of the invention. The peptides have neuronal exocytosis
 CC inhibitory activity and are used for treatment of facial wrinkles and
 CC asymmetry and pathological neuronal exocytosis-mediated pathological
 CC disorders and alterations manifested e.g. by spasms and neurological and
 CC neurodegenerative disorders
 XX Sequence 86 AA;
 SQ Query Match 100.0%; Score 89; DB 4; Length 86;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 DB 60 RIMEKADSNKTRIDEANQ 77
 RESULT 7
 ID AAO15165 standard; peptide; 116 AA.
 XX AAO15165;
 AC AAO15165;
 XX 02-SEP-2002 (first entry)
 DT Clostridial neurotoxin protease substrate peptide 4.
 DE Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
 KW fluorescence resonant energy transfer assay; quenched-signal;
 KW clostridial neurotoxin detection; food.
 XX Unidentified.
 OS Key Location/Qualifiers
 XX Modified-site 1 /note= "S-fluoresceinyl-cysteine"
 FT Cleavage-site 89..90
 FT /note= "The peptide is cleaved between these two residues
 FT by type E Clostridium botulinum neurotoxin"

FT Cleavage-site 106..107
 FT /note= "The peptide is cleaved between these two residues
 FT by type A Clostridium botulinum neurotoxin"
 XX WO200225284-A2.
 XX 28-MAR-2002.
 XX 25-SEP-2001; 2001WO-US030188.
 XX 25-SEP-2000; 2000US-0235050P.
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 XX Schmidt JJ, Stafford RG;
 XX WPI; 2002-499829/53.
 XX Substrate useful in e.g. an assay for the protease activity of
 PT clostridial neurotoxin, comprises modified peptide or protein.
 XX Claim 22; Page 16; 48pp; English.
 XX The invention comprises clostridial neurotoxin substrate peptides which
 CC can serve as fluorescence resonant energy transfer assay (FRET) or
 CC quenched-signal substrates in assays for the proteolytic activities of
 CC clostridial neurotoxins. The invention further comprises Clostridium
 CC botulinum neurotoxin substrate peptides that can serve as immobilised
 CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
 CC activities of clostridial neurotoxins. The clostridial (including the
 CC Clostridium botulinum) neurotoxin substrate peptides are useful for
 CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
 CC or an environmental sample). The present amino acid sequence represents a
 CC clostridial neurotoxin substrate peptide of the invention
 XX Sequence 116 AA;
 SQ Query Match 100.0%; Score 89; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 DB 89 RIMEKADSNKTRIDEANQ 106
 RESULT 8
 ID AAO15166 standard; peptide; 116 AA.
 XX AAO15166;
 AC AAO15166;
 XX 02-SEP-2002 (first entry)
 DT Clostridial neurotoxin protease substrate peptide 5.
 DE Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
 KW fluorescence resonant energy transfer assay; quenched-signal;
 KW clostridial neurotoxin detection; food.
 XX Unidentified.
 OS Key Location/Qualifiers
 XX Modified-site 1 /note= "S-fluoresceinyl-cysteine"
 FT Cleavage-site 89..90
 FT /note= "The peptide is cleaved between these two residues
 FT by type E Clostridium botulinum neurotoxin"

WO200225284-A2.
 28-MAR-2002.

XX 25-SEP-2001; 2001WO-US030188.
 XX 25-SEP-2000; 2000US-0235050P.
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 XX Schmidt JJ, Stafford RG;
 XX WPI; 2002-499829/53.
 XX Substrate useful in e.g. an assay for the protease activity of
 PT clostridial neurotoxin, comprises modified peptide or protein.
 PT Claim 28; Page 17; 48pp; English.
 XX The invention comprises clostridial neurotoxin substrate peptides which
 CC can serve as fluorescence resonant energy transfer assay (FRET) or
 CC quenched-signal substrates in assays for the proteolytic activities of
 CC clostridial neurotoxins. The invention further comprises Clostridium
 CC botulinum neurotoxin substrate peptides that can serve as immobilised
 CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
 CC activities of clostridial neurotoxins. The clostridial (including the
 CC Clostridium botulinum) neurotoxin substrate peptides are useful for
 CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
 CC or an environmental sample). The present amino acid sequence represents a
 CC clostridial neurotoxin substrate peptide of the invention
 XX
 SQ Sequence 116 AA;
 Query Match 100.0%; Score 89; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 Db 89 RIMEKADSNKTRIDEANQ 106
 |||||
 RESULT 9
 AAU00255
 ID AAU00255 standard; protein; 198 AA.
 AC AAU00255;
 XX 12-SEP-2001 (first entry)
 DT Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX Mus sp.
 OS Synthetic.
 XX WO200118038-A2.
 FN 15-MAR-2001.
 PD 18-AUG-2000; 2000WO-GB003196.
 PF 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state. Note: The present sequence is
 CC not shown in the specification but is derived from the mouse SNAP-25
 CC sequence given in figure 8 (see AAU00246)
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 89; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 Db 180 RIMEKADSNKTRIDEANQ 197
 |||||
 RESULT 10
 AAU00263
 ID AAU00263 standard; protein; 199 AA.
 AC AAU00263;
 XX 12-SEP-2001 (first entry)
 DT Synaptosomal-associated protein, SNAP25, mutant 1-199 (R198T).
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 XX WO200118038-A2.
 FN 15-MAR-2001.
 PD 18-AUG-2000; 2000WO-GB003196.
 PF 20-AUG-1999; 99US-0149993P.
 XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 XX associated protein, SNAP25, mutant 1-199(R198T), used in a new method of
 XX treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX or a recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state. Note: The present sequence is not shown in the specification but
 XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX AAU00246)
 XX
 XX Sequence 199 AA;
 XX
 XX Query Match 100.0%; Score 89; DB 4; Length 199;
 XX Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RIMEKADSNKTRIDEANQ 18
 XX |||||
 XX Db 180 RIMEKADSNKTRIDEANQ 197
 XX
 XX RESULT 11
 XX AAU00264
 XX ID AAU00264 standard; protein; 200 AA.
 XX AC AAU00264;
 XX
 XX 12-SEP-2001 (first entry)
 XX
 XX Synaptosomal-associated protein, SNAP25, mutant 1-200(R198T).
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX synaptosomal-associated protein; mouse; mutant; mutein;
 XX N-ethylmaleimide-sensitive fusion protein;
 XX soluble NSF-attachment protein receptor.
 XX
 XX Mus sp.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT Misc-difference 198
 XX /note= "Wild-type Arg substituted by Thr"
 XX
 XX WO200118038-A2.
 XX PN

XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 XX associated protein, SNAP25, mutant 1-200(R198T), used in a new method of
 XX treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX or a recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state. Note: The present sequence is not shown in the specification but
 XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX AAU00246)
 XX
 XX Sequence 200 AA;
 XX
 XX Query Match 100.0%; Score 89; DB 4; Length 200;
 XX Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RIMEKADSNKTRIDEANQ 18
 XX |||||
 XX Db 180 RIMEKADSNKTRIDEANQ 197
 XX
 XX RESULT 12
 XX AAU02637
 XX ID AAU02637 standard; protein; 201 AA.
 XX AC AAU02637;
 XX
 XX 12-SEP-2001 (first entry)
 XX
 XX Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX synaptosomal-associated protein; mouse; mutant; mutein;
 XX N-ethylmaleimide-sensitive fusion protein;
 XX soluble NSF-attachment protein receptor.
 XX
 XX Mus sp.

OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT
 FT
 XX WO200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 XX Sequence 201 AA;
 SQ
 Query Match 100.0%; Score 89; DB 4; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 Db ||||||||||||||||
 180 RIMEKADSNKTRIDEANQ 197
 RESULT 13
 AAU00265
 ID AAU00265 standard; protein; 202 AA.
 XX
 XX AAU00265;
 XX
 XX 12-SEP-2001 (first entry)
 XX
 XX Synaptosomal-associated protein, SNAP25, mutant 1-202 (R198T).
 DE

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX Mus sp.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT
 FT
 XX WO200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-202(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 XX Sequence 202 AA;
 SQ
 Query Match 100.0%; Score 89; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 Db ||||||||||||||||
 180 RIMEKADSNKTRIDEANQ 197
 RESULT 14
 AAU02636
 ID AAU02636 standard; protein; 203 AA.

XX AC AAU02636;
 XX DT 12-SEP-2001 (first entry)
 XX DE Synaptosomal-associated protein, SNAP25, mutant 1-203 (R198T).
 XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX OS Mus sp.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT WT
 FN WC200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WC-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX DR WPI; 2001-226739/23.
 XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX SQ Sequence 203 AA;
 XX Query Match 100.0%; Score 89; DB 4; Length 203;
 XX Best Local Similarity 100.0%; Pred. No. 3.5e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 RIMEKADSNKTRIDEANQ 18
 XX |||||||||||||||||||
 XX DB 180 RIMEKADSNKTRIDEANQ 197
 XX |||||||||||||||||||
 XX Query Match 100.0%; Score 89; DB 2; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 RIMEKADSNKTRIDEANQ 18
 XX |||||||||||||||||||
 XX DB 180 RIMEKADSNKTRIDEANQ 197
 XX |||||||||||||||||||
 XX Search completed: March 9, 2004, 11:07:36
 XX Job time : 50.6216 secs

DB 180 RIMEKADSNKTRIDEANQ 197
 |||||||||||||||||||
 RESULT 15
 AAW30103
 ID AAW30103 standard; peptide; 206 AA.
 XX AAW30103;
 AC AAW30103;
 XX 06-APR-1998 (first entry)
 DT 06-APR-1998 (first entry)
 XX Synaptosomal associated protein.
 DE Synaptosomal associated protein.
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WC9734620-A1.
 FN WC9734620-A1.
 XX PD 25-SEP-1997.
 XX PF 18-MAR-1997; 97WO-US004393.
 XX PR 18-MAR-1996; 96US-0013599P.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Montal M;
 XX DR WPI; 1997-479986/44.
 XX PT Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neurotransmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX PS Disclosure; Page 27-28; 61pp; English.
 XX CC This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 microm, especially 0.25 microm, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neuronal cells provide targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX SQ Sequence 206 AA;
 XX Query Match 100.0%; Score 89; DB 2; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 RIMEKADSNKTRIDEANQ 18
 XX |||||||||||||||||||
 XX DB 180 RIMEKADSNKTRIDEANQ 197
 XX |||||||||||||||||||